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(54) Title: RECOMBINANT VESICULOVIRUSES AND THEIR USES			
(57) Abstract The present invention provides recombinant replicable vesiculoviruses. The invention provides a method which, for the first time, successfully allows the production and recovery of replicable vesiculoviruses, as well as recombinant replicable vesiculoviruses, from cloned DNA, by a method comprising expression of the full-length positive-strand vesiculovirus antigenomic RNA in host cells. The recombinant vesiculoviruses do not cause serious pathology in humans, can be obtained in high titers, and have use as vaccines. The recombinant vesiculoviruses can also be inactivated for use as killed vaccines.			

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RECOMBINANT VESICULOVIRUSES AND THEIR USES

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1. INTRODUCTION

The present invention relates to recombinant vesiculoviruses which are replicable and capable of expressing foreign nucleic acid contained in their genome. Also provided are inactivated forms of the recombinant viruses. The vesiculoviruses are useful in vaccine formulations to prevent or treat various diseases and disorders.

2. BACKGROUND OF THE INVENTION2.1. RHABDOVIRUSES

Rhabdoviruses are membrane-enveloped viruses that are widely distributed in nature where they infect vertebrates, invertebrates, and plants. There are two distinct genera within the rhabdoviruses, the Lyssavirus genus and the Vesiculovirus genus. Rhabdoviruses have single, negative-strand RNA genomes of 11-12,000 nucleotides (Rose and Schubert, 1987, Rhabdovirus genomes and their products, in *The Viruses: The Rhabdoviruses*, Plenum Publishing Corp., NY, pp. 129-166). The virus particles contain a helical, nucleocapsid core composed of the genomic RNA and protein. Generally, three proteins, termed N (nucleocapsid), P (formerly termed NS, originally indicating nonstructural), and L (large) are found to be associated with the nucleocapsid. An additional matrix (M) protein lies within the membrane envelope, perhaps interacting both with the membrane and the nucleocapsid core. A single glycoprotein (G) species spans the membrane and forms the spikes on the surface of the virus particle. Because the genome is the negative sense [i.e., complementary to the RNA

sequence (positive sense) that functions as mRNA to directly produce encoded protein], rhabdoviruses must encode and package an RNA-dependent RNA polymerase in the virion (Baltimore et al., 1970, Proc. Natl. Acad. Sci. USA 66: 5 572-576), composed of the P and L proteins. This enzyme transcribes genomic RNA to make subgenomic MRNAs encoding the 5-6 viral proteins and also replicates full-length positive and negative sense RNAs. The genes are transcribed sequentially, starting at the 3' end of the genomes. The 10 same basic genetic system is also employed by the paramyxoviruses and filoviruses.

The prototype rhabdovirus, vesicular stomatitis virus (VSV), grows to very high titers in most animal cells and can be prepared in large quantities. As a result, VSV 15 has been widely used as a model system for studying the replication and assembly of enveloped RNA viruses. The study of VSV and related negative strand viruses has been limited by the inability to perform direct genetic manipulation of the virus using recombinant DNA technology. The difficulty 20 in generating VSV from DNA is that neither the full-length genomic nor antigenomic RNAs are infectious. The minimal infectious unit is the genomic RNA tightly bound to 1,250 subunits of the nucleocapsid (N) protein (Thomas et al., 1985, J. Virol. 54:598-607) and smaller amounts of the two 25 virally encoded polymerase subunits, L and P. To reconstitute infectious virus from the viral RNA, it is necessary first to assemble the N protein-RNA complex that serves as the template for transcription and replication by the VSV polymerase. Although smaller negative-strand RNA 30 segments of the influenza virus genome can be packaged into nucleocapsids *in vitro*, and then rescued in influenza infected cells (Enami et al., 1990, Proc. Natl. Acad. Sci. USA 87:3802-3805; Luytjes et al., 1989, Cell 59:1107-1113), systems for packaging the much larger rhabdoviral genomic 35 RNAs *in vitro* are not yet available.

Recently, systems for replication and transcription of DNA-derived minigenomes or small defective RNAs from

rhabdoviruses (Conzelmann and Schnell, 1994, J. Virol. 68:713-719; Pattnaik et al., 1992, Cell 69:1011-1120) and paramyxoviruses (Calain et al., 1992, Virology 191:62-71; Collins et al., 1991, Proc. Natl. Acad. Sci. USA 88:9663-9667; Collins et al., 1993, Virology 195:252-256; De and Banerjee, 1993, Virology 196:344-348; Dimock and Collins, 1993, J. Virol. 67:2772-2778; Park et al., 1991, Proc. Natl. Acad. Sci. USA 88:5537-5541) have been described. In these systems, RNAs are assembled into nucleocapsids within cells that express the viral N protein and polymerase proteins. Although these systems have been very useful, they do not allow genetic manipulation of the full-length genome of infectious viruses.

The recovery of rabies virus from a complete cDNA clone was published recently (Schnell et al., 1994, EMBO J. 13:4195-4203). The infectious cycle was initiated by expressing the antigenomic (full-length positive strand) RNA in cells expressing the viral N, P, and L proteins. Although rabies virus is a rhabdovirus, it is structurally and functionally different from the vesiculoviruses. Rabies virus is a Lyssavirus, not a Vesiculovirus. Lyssaviruses invade the central nervous system. Vesiculoviruses invade epithelial cells, predominantly those of the tongue, to produce vesicles. Rabies virus causes encephalitis in a variety of animals and in humans, while VSV causes an epidemic but self-limiting disease in cattle. In sharp contrast to VSV-infected cells, rabies virus produces little or no cytopathic effect in infected cell culture, replicates less efficiently than VSV in cell culture, and causes little depression of cellular DNA, RNA or protein synthesis in infected cell cultures (see Baer et al., 1990, in Virology, 2d ed., Fields et al. (eds.), Raven Press, Ltd., NY, pp. 883, 887). Indeed, there is no cross-hybridization observed between the genomes of rabies virus and VSV, and sequence homology between the two genomes is generally discernable only with the aid of computer run homology programs. The differences between vesiculoviruses and rabies virus, and the

extremely rare nature of rabies virus recovery from cDNA ($\sim 10^8$ cells are transfected to yield one infectious cell), renders it unpredictable whether the strategy used with rabies virus would be successful for viruses of a different genus, i.e.,
5 the vesiculoviruses.

The recovery of infectious measles virus, another negative strand RNA virus, from cloned cDNA has been attempted, without success (see Ballart et al., 1990, EMBO J. 9(2):379-384 and the retraction thereof by Eschle et al.,
10 1991, EMBO J. 10(11):3558).

2.2. VACCINES

The development of vaccines for the prevention of viral, bacterial, or parasitic diseases is the focus of much
15 research effort.

Traditional ways of preparing vaccines include the use of inactivated or attenuated pathogens. A suitable inactivation of the pathogenic microorganism renders it harmless as a biological agent but does not destroy its
20 immunogenicity. Injection of these "killed" particles into a host will then elicit an immune response capable of preventing a future infection with a live microorganism. However, a major concern in the use of killed vaccines (using inactivated pathogen) is failure to inactivate all the
25 microorganism particles. Even when this is accomplished, since killed pathogens do not multiply in their host, or for other unknown reasons, the immunity achieved is often incomplete, short lived and requires multiple immunizations. Finally, the inactivation process may alter the
30 microorganism's antigens, rendering them less effective as immunogens.

Attenuation refers to the production of strains of pathogenic microorganisms which have essentially lost their disease-producing ability. One way to accomplish this is to
35 subject the microorganism to unusual growth conditions and/or frequent passage in cell culture. Mutants are then selected which have lost virulence but yet are capable of eliciting an

immune response. Attenuated pathogens often make good immunogens as they actually replicate in the host cell and elicit long lasting immunity. However, several problems are encountered with the use of live vaccines, the most worrisome 5 being insufficient attenuation and the risk of reversion to virulence.

An alternative to the above methods is the use of subunit vaccines. This involves immunization only with those components which contain the relevant immunological material.

10 Vaccines are often formulated and inoculated with various adjuvants. The adjuvants aid in attaining a more durable and higher level of immunity using small amounts of antigen or fewer doses than if the immunogen were administered alone. The mechanism of adjuvant action is 15 complex and not completely understood. However, it may involve the stimulation of cytokine production, phagocytosis and other activities of the reticuloendothelial system as well as a delayed release and degradation of the antigen. Examples of adjuvants include Freund's adjuvant (complete or 20 incomplete), Adjuvant 65 (containing peanut oil, mannide monooleate and aluminum monostearate), the pluronic polyol L-121, Avridine, and mineral gels such as aluminum hydroxide, aluminum phosphate, etc. Freund's adjuvant is no longer used in vaccine formulations for humans because it contains 25 nonmetabolizable mineral oil and is a potential carcinogen.

3. SUMMARY OF THE INVENTION

The present invention provides recombinant replicable vesiculoviruses. The prior art has unsuccessfully 30 attempted to produce replicable vesiculoviruses from cloned DNA. In contrast, the invention provides a method which, for the first time, has successfully allowed the production and recovery of replicable vesiculoviruses, as well as recombinant replicable vesiculoviruses, from cloned DNA.

35 The vesiculoviruses of the invention are produced by providing in an appropriate host cell: (a) DNA that can be transcribed to yield (encodes) vesiculovirus antigenomic

(+) RNA (complementary to the vesiculovirus genome), (b) a recombinant source of vesiculovirus N protein, (c) a recombinant source of vesiculovirus P protein, and (d) a recombinant source of vesiculovirus L protein; under
5 conditions such that the DNA is transcribed to produce the antigenomic RNA, and a vesiculovirus is produced that contains genomic RNA complementary to the antigenomic RNA produced from the DNA.

The invention provides an infectious recombinant
10 vesiculovirus capable of replication in an animal into which the recombinant vesiculovirus is introduced, in which the genome of the vesiculovirus comprises foreign RNA which is not naturally a part of the vesiculovirus genome. The recombinant vesiculovirus is formed by producing
15 vesiculoviruses according to the method of the invention, in which regions of the DNA encoding vesiculovirus antigenomic (+) RNA that are nonessential for viral replication have been inserted into or replaced with foreign DNA.

In a preferred embodiment, the foreign RNA
20 contained within the genome of the recombinant vesiculovirus (originally encoded by the foreign DNA), upon expression in an appropriate host cell, produces a protein or peptide that is antigenic or immunogenic.

The recombinant vesiculoviruses of the invention
25 have use as vaccines. In one embodiment, where the foreign RNA directs production of an antigen that induces an immune response against a pathogen, the vaccines of the invention have use in the treatment or prevention of infections by such a pathogen (particularly a pathogenic microorganism), and its
30 clinical manifestations, i.e., infectious disease. In a preferred embodiment, such an antigen displays the antigenicity or immunogenicity of an envelope glycoprotein of a virus other than a vesiculovirus, and the antigen is incorporated into the vesiculovirus envelope. The
35 recombinant vesiculoviruses also have uses in diagnosis, and monitoring progression of infectious disorders, including response to vaccination and/or therapy.

In another embodiment, where the foreign RNA directs production of an antigen that induces an immune response against a tumor, the recombinant viruses of the invention have uses in cancer immunoprophylaxis, immunotherapy, and diagnosis, and monitoring of tumor progression or regression.

The recombinant vesiculoviruses can be used as live vaccines, or can be inactivated for use as killed vaccines. The recombinant viruses can also be used to produce large quantities of readily purified antigen, e.g., for use in subunit vaccines.

The invention also provides vaccine formulations, kits, and recombinant host cells.

15

4. DESCRIPTION OF THE FIGURES

Figure 1. Nucleotide sequence of plasmid pVSVFL(+), showing the complete DNA sequence that is transcribed to produce VSV antigenomic (+) RNA, and predicted sequences of the encoded VSV proteins. [N protein: SEQ ID NO:2; P protein: SEQ ID NO:3; M protein: SEQ ID NO:4; G protein: SEQ ID NO:5; L protein: SEQ ID NO:6] The noncoding and intergenic regions are observable. The upper line of sequence (SEQ ID NO:1) is the VSV antigenomic positive strand; lower line = SEQ ID NO:7. Restriction sites are indicated. The transmembrane and cytoplasmic domains of the G protein are also indicated. The sequences of the first T7 RNA polymerase promoter (SEQ ID NO:8), the second T7 RNA polymerase promoter (SEQ ID NO:9); leader sequence (SEQ ID NO:10), T7 RNA polymerase transcription termination signal (SEQ ID NO:11), and the sequence that is transcribed to produce the HDV ribozyme (SEQ ID NO:12) are shown.

Figure 2. Nucleotide sequence of a portion of plasmid pVSVSS1, showing the synthetic DNA insert containing the polylinker region inserted between the G and L coding regions (3' of G and 5' of L) containing unique restriction enzyme recognition sites, namely, XmaI, NotI, and SmaI.

Upper line of sequence: SEQ ID NO:13; lower line of sequence: SEQ ID NO:14.

Figure 3. Gene junctions of VSV. The nucleotide sequences at the 3' end of the leader RNA and the 5' and 3' ends of each mRNA are shown along with the corresponding genomic sequences (VRNA) (SEQ ID NO:15-31). The intergenic dinucleotides are indicated by bold letters. From Rose and Schubert, 1987, in *The Viruses: The Rhabdoviruses*, Plenum Press, NY, pp. 129-166, at p. 136.

10 Figure 4. Plasmid DNA construction. A. The diagram illustrates the cloned VSV genomic sequence and the four DNA fragments (numbered 1-4) that were used to generate the plasmid pVSVFL(+). The horizontal arrows represent PCR primers used to generate fragments 1 and 3. B. Diagram of
15 the plasmid pVSVFL(+) that gives rise to infectious VSV. The locations of the VSV genes encoding the five proteins N, P, M, G, and L are shown. The stippled region from Sac I to Xho I represents the pBSSK⁺ vector sequence, and the hatched segments represent the regions of the VSV genome generated by
20 PCR. Transcription from the T7 promoter generates the complete (+) strand VSV RNA.

Figure 5. Proteins present in wild-type and recombinant VSVs. Proteins from 1% of the virus recovered from approximately 5×10^6 infected BHK cells were separated
25 by SDS-PAGE (10% acrylamide) and visualized by staining with Coomassie brilliant blue. Positions of the five VSV proteins are indicated.

Figure 6. Identification of a restriction enzyme recognition sequence in the recombinant VSV. A 620
30 nucleotide segment of genomic RNA isolated from wildtype and recombinant VSV was amplified by reverse transcription and PCR using the primers 5'-CATTCAGACGCTGCTTCGCAACTTCC (SEQ ID NO:32) and 5'-CATGAATGTTAACATCTCAAGA (SEQ ID NO:33). Controls in which reverse transcriptase was omitted from the
35 reaction are indicated. DNA samples were either digested with Nhe I or left undigested prior to electrophoresis on a 6% polyacrylamide gel as indicated. DNA was detected by

staining with ethidium bromide. Sizes of DNA markers are indicated on the left.

Figure 7: Autoradiogram showing the sequence of genomic RNA from recombinant VSV. RNA prepared from 5 recombinant VSV was sequenced by the dideoxy method using reverse transcriptase. The written sequence corresponds to nucleotides 1563-1593 in the G mRNA (Rose and Gallione, 1981, J. Virol. 39:519-528). The underlined sequence represents the four nucleotides that were changed to generate the Nhe I 10 site.

Figure 8. Protein analysis of recombinant VSV expressing the glycoprotein from the New Jersey serotype. Proteins from 1% of the virus pelleted from the medium of approximately 5×10^6 BHK cells infected for 24 hours with 15 wildtype VSV_I (lane 1), recombinant VSV_{INIG} (lane 2) or wildtype VSV_{NJ} (lane 3) were separated by SDS-PAGE (10% acrylamide). The proteins were visualized by staining with Coomassie brilliant blue. Positions of viral proteins are indicated.

20

5. DETAILED DESCRIPTION OF THE INVENTION

The present invention provides recombinant replicable vesiculoviruses. The prior art has unsuccessfully attempted to produce replicable vesiculoviruses from cloned DNA. In contrast, the invention provides a method which, for 25 the first time, has successfully allowed the production and recovery of replicable vesiculoviruses, as well as recombinant replicable vesiculoviruses, from cloned DNA. Expression of the full-length positive-strand vesiculovirus RNA in host cells has successfully allowed the generation of 30 recombinant vesiculoviruses from DNA, providing recombinant viruses that do not cause serious pathology in humans and that can be obtained in high titers, that have use as vaccines.

The vesiculoviruses of the invention are produced 35 by providing in an appropriate host cell: (a) DNA that can be transcribed to yield (encodes) vesiculovirus antigenomic (+) RNA (complementary to the vesiculovirus genome), (b) a

recombinant source of vesiculovirus N protein, (c) a recombinant source of vesiculovirus P protein, and (d) a recombinant source of vesiculovirus L protein; under conditions such that the DNA is transcribed to produce the antigenomic RNA, and a vesiculovirus is produced that contains genomic RNA complementary to the antigenomic RNA produced from the DNA.

The invention provides an infectious recombinant vesiculovirus capable of replication in an animal into which the recombinant vesiculovirus is introduced, in which the genome of the vesiculovirus comprises foreign RNA which is not naturally a part of the vesiculovirus genome. The recombinant vesiculovirus is formed by producing vesiculoviruses according to the method of the invention, in which regions of the DNA encoding vesiculovirus antigenomic (+) RNA that are nonessential for viral replication have been inserted into or replaced with foreign DNA.

Since the viruses are replicable (i.e., not replication-defective), they encode all the vesiculovirus machinery necessary for replication in a cell upon infection by the virus.

In a preferred embodiment, the recombinant vesiculovirus is a recombinant vesicular stomatitis virus (VSV).

In another preferred embodiment, the foreign RNA contained within the genome of the recombinant vesiculovirus (originally encoded by the foreign DNA), upon expression in an appropriate host cell, produces a protein or peptide that is antigenic or immunogenic. Such an antigenic or immunogenic protein or peptide whose expression is directed by the foreign RNA (present in the negative sense) within the vesiculovirus genome (by expression from the (+) antigenomic message) shall be referred to hereinafter as the "Antigen." Appropriate Antigens include but are not limited to known antigens of pathogenic microorganisms or of tumors, as well as fragments or derivatives of such antigens displaying the antigenicity or immunogenicity of such antigens. A protein

displays the antigenicity of an antigen when the protein is capable of being immunospecifically bound by an antibody to the antigen. A protein displays the immunogenicity of an antigen when it elicits an immune response to the antigen (e.g., when immunization with the protein elicits production of an antibody that immunospecifically binds the antigen or elicits a cell-mediated immune response directed against the antigen).

The recombinant vesiculoviruses of the invention have use as vaccines. In one embodiment, where the foreign RNA directs production of an Antigen (originally encoded by the foreign DNA used to produce the recombinant vesiculovirus or its predecessor) that induces an immune response against a pathogen, the vaccines of the invention have use in the treatment or prevention of infections by such a pathogen (particularly a pathogenic microorganism), and its clinical manifestations, i.e., infectious disease. The invention thus provides methods of prevention or treatment of infection and infectious disease comprising administering to a subject in which such treatment or prevention is desired one or more of the recombinant vesiculoviruses of the invention. The recombinant vesiculoviruses also have uses in diagnosis, and monitoring progression of infectious disorders, including response to vaccination and/or therapy.

In another embodiment, where the Antigen induces an immune response against a tumor, the recombinant viruses of the invention have uses in cancer immunoprophylaxis, immunotherapy, and diagnosis, and monitoring of tumor progression or regression.

The recombinant vesiculoviruses can be used as live vaccines, or can be inactivated for use as killed vaccines. The recombinant viruses can also be used to produce large quantities of readily purified antigen, e.g., for use in subunit vaccines.

In a specific embodiment, the foreign DNA used initially for production of the recombinant vesiculoviruses can also comprise a sequence encoding a detectable marker,

e.g., β -galactosidase, β -glucuronidase, β -geo (Friedrich & Soriano, 1991, Genes Dev. 5:1513-1523).

In another specific embodiment, the foreign DNA can also comprise a sequence encoding a cytokine capable of
5 stimulating an immune response. Such cytokines include but are not limited to, interleukin-2, interleukin-6, interleukin-12, interferons, and granulocyte-macrophage colony stimulating factors.

In a preferred aspect, upon infection with a
10 recombinant vesiculovirus of the invention, the Antigen is expressed as a nonfusion protein. In a less preferred embodiment, the Antigen is expressed as a fusion protein, e.g., to the viral G protein. "Fusion protein," as used herein, refers to a protein comprising an amino acid sequence
15 from a first protein covalently linked via a peptide bond at its carboxy terminus to the amino terminus of an amino acid sequence from a second, different protein.

In one embodiment, a vaccine formulation of the invention contains a single type of recombinant vesiculovirus
20 of the invention. In another embodiment, a vaccine formulation comprises a mixture of two or more recombinant viruses of the invention.

The vaccine formulations of the invention provide one or more of the following benefits: stability for long
25 periods without refrigeration; ease of production; low cost and high titer of production; ability to be administered by local workers without advanced medical training; and involving administration of a microorganism that is known not to cause serious disease in humans.

30 The present invention also provides a host cell infected with a recombinant vesiculovirus capable of replication. In one embodiment, the host cell is a mammalian cell. Preferably, the mammalian cell is a hamster kidney cell.

35

5.1. DNA THAT CAN BE TRANSCRIBED TO PRODUCE
VESICULOVIRUS ANTIGENOMIC (+) RNA

Many vesiculoviruses are known in the art and can be made recombinant according to the methods of the invention. Examples of such vesiculoviruses are listed in Table I.

TABLE I

MEMBERS OF THE VESICULOVIRUS GENUS

	<u>Virus</u>	<u>Source of virus in nature</u>
	VSV-New Jersey	Mammals, mosquitoes, midges, blackflies, houseflies
	VSV-Indiana	Mammals, mosquitoes, sandflies
15	Alagoas	Mammals, sandflies
	Cocal	Mammals, mosquitoes, mites
	Jurona	Mosquitoes
	Carajas	Sandflies
20	Maraba	Sandflies
	Piry	Mammals
	Calchaqui	Mosquitoes
25	Yug Bogdanovac	Sandflies
	Isfahan	Sandflies, ticks
	Chandipura	Mammals, sandflies
	Perinct	Mosquitoes, sandflies
30	Porton-S	Mosquitoes

Any DNA that can be transcribed to produce vesiculovirus antigenomic (+) RNA (complementary to the VSV genome) can be used for the construction of a recombinant DNA containing foreign DNA encoding an Antigen; for use in

producing the recombinant vesiculoviruses of the invention. DNA that can be transcribed to produce vesiculovirus antigenomic (+) RNA (such DNA being referred to herein as "vesiculovirus (-) DNA") is available in the art and/or can
5 be obtained by standard methods. In particular, plasmid pVSVFL(+), containing VSV (-) DNA that is preferred for use in the present invention, has been deposited with the ATCC and assigned accession no. 97134. In a preferred aspect, DNA that can be transcribed to produce VSV (+) RNA, [i.e.,
10 VSV (-) DNA], is used. VSV (-) DNA for any serotype or strain known in the art, e.g., the New Jersey or Indiana serotypes of VSV, can be used. The complete nucleotide and deduced protein sequence of the VSV genome is known, and is available as Genbank VSVCG, Accession No. J02428; NCBI Seq ID
15 335873; and is published in Rose and Schubert, 1987, in *The Viruses: The Rhabdoviruses*, Plenum Press, NY, pp. 129-166. Partial sequences of other vesiculovirus genomes have been published and are available in the art. The complete sequence of the VSV(-) DNA that is used in a preferred
20 embodiment is contained in plasmid pVSVFL(+) and is shown in Figure 1; also shown are with the predicted sequences of the VSV proteins (this sequence contains several sequence corrections relative to that obtainable from Genbank). Vesiculovirus (-) DNA, if not already available, can be
25 prepared by standard methods, as follows: If vesiculoviral cDNA is not already available, vesiculovirus genomic RNA can be purified from virus preparations, and reverse transcription with long distance polymerase chain reaction used to generate the vesiculovirus (-) DNA. Alternatively,
30 after purification of genomic RNA, VSV mRNA can be synthesized *in vitro*, and cDNA prepared by standard methods, followed by insertion into cloning vectors (see, e.g., Rose and Gallione, 1981, *J. Virol.* 39(2):519-528). Individual cDNA clones of vesiculovirus RNA can be joined by use of
35 small DNA fragments covering the gene junctions, generated by use of reverse transcription and polymerase chain reaction (RT-PCR) (Mullis and Faloona, 1987, *Meth. Enzymol.*

155:335-350) from VSV genomic RNA (see Section 6, *infra*). Vesiculoviruses are available in the art. For example, VSV can be obtained from the American Type Culture Collection.

In a preferred embodiment, one or more, preferably
5 unique, restriction sites (e.g., in a polylinker) are introduced into the vesiculovirus (-) DNA, in intergenic regions, or 5' of the sequence complementary to the 3' end of the vesiculovirus genome, or 3' of the sequence complementary to the 5' end of the vesiculovirus genome, to facilitate
10 insertion of the foreign DNA.

In a preferred method of the invention, the vesiculovirus (-) DNA is constructed so as to have a promoter operatively linked thereto. The promoter should be capable of initiating transcription of the (-) DNA in an animal or
15 insect cell in which it is desired to produce the recombinant vesiculovirus. Promoters which may be used include, but are not limited to, the SV40 early promoter region (Bernoist and Chambon, 1981, Nature 290:304-310), the promoter contained in the 3' long terminal repeat of Rous sarcoma virus (Yamamoto,
20 et al., 1980, Cell 22:787-797), the herpes thymidine kinase promoter (Wagner et al., 1981, Proc. Natl. Acad. Sci. U.S.A. 78:1441-1445), the regulatory sequences of the metallothionein gene (Brinster et al., 1982, Nature 296:39-42); heat shock promoters (e.g., hsp70 for use in
25 *Drosophila* S2 cells); the ADC (alcohol dehydrogenase) promoter, PGK (phosphoglycerol kinase) promoter, alkaline phosphatase promoter, and the following animal transcriptional control regions, which exhibit tissue specificity and have been utilized in transgenic animals:
30 elastase I gene control region which is active in pancreatic acinar cells (Swift et al., 1984, Cell 38:639-646; Ornitz et al., 1986, Cold Spring Harbor Symp. Quant. Biol. 50:399-409; MacDonald, 1987, Hepatology 7:425-515); insulin gene control region which is active in pancreatic beta cells (Hanahan,
35 1985, Nature 315:115-122), immunoglobulin gene control region which is active in lymphoid cells (Grosschedl et al., 1984, Cell 38:647-658; Adames et al., 1985, Nature 318:533-538;

Alexander et al., 1987, Mol. Cell. Biol. 7:1436-1444), mouse mammary tumor virus control region which is active in testicular, breast, lymphoid and mast cells (Leder et al., 1986, Cell 45:485-495), albumin gene control region which is
5 active in liver (Pinkert et al., 1987, Genes and Devel. 1:268-276), alpha-fetoprotein gene control region which is active in liver (Krumlauf et al., 1985, Mol. Cell. Biol. 5:1639-1648; Hammer et al., 1987, Science 235:53-58; alpha 1-antitrypsin gene control region which is active in the liver
10 (Kelsey et al., 1987, Genes and Devel. 1:161-171), beta-globin gene control region which is active in myeloid cells (Mogram et al., 1985, Nature 315:338-340; Kollias et al., 1986, Cell 46:89-94; myelin basic protein gene control region which is active in oligodendrocyte cells in the brain
15 (Readhead et al., 1987, Cell 48:703-712); and myosin light chain-2 gene control region which is active in skeletal muscle (Sani, 1985, Nature 314:283-286). Preferably, the promoter is an RNA polymerase promoter, preferably a bacteriophage or viral or insect RNA polymerase promoter,
20 including but not limited to the promoters for T7 RNA polymerase, SP6 RNA polymerase, and T3 RNA polymerase. If an RNA polymerase promoter is used in which the RNA polymerase is not endogenously produced by the host cell in which it is desired to produce the recombinant vesiculovirus, a
25 recombinant source of the RNA polymerase must also be provided in the host cell.

The vesiculovirus (-) DNA can be operably linked to a promoter before or after insertion of foreign DNA encoding an Antigen. Preferably, a transcriptional terminator is
30 situated downstream of the vesiculovirus (-) DNA.

In another preferred embodiment, a DNA sequence that can be transcribed to produce a ribozyme sequence is situated at the immediate 3' end of the vesiculovirus (-) DNA, prior to the transcriptional termination signal, so that
35 upon transcription a self-cleaving ribozyme sequence is produced at the 3' end of the antigenomic RNA, which ribozyme sequence will autolytically cleave (after a U) this fusion

transcript to release the exact 3' end of the vesiculovirus antigenomic (+) RNA. Any ribozyme sequence known in the art may be used, as long as the correct sequence is recognized and cleaved. (It is noted that hammerhead ribozyme is probably not suitable for use.) In a preferred aspect, hepatitis delta virus (HDV) ribozyme is used (Perrotta and Been, 1991, Nature 350:434-436; Pattnaik et al., 1992, Cell 69:1011-1020).

A preferred VSV(-) DNA for use, for insertion of foreign DNA, is that shown in Fig. 1 and contained in plasmid pVSVFL(+), in which a T7 RNA polymerase promoter is present 5' of the sequence complementary to the 3' end of the VSV genome. Plasmid pVSVFL(+) thus comprises (in 5' to 3' order) the following operably linked components: the T7 RNA polymerase promoter, VSV (-) DNA, a DNA sequence that is transcribed to produce an HDV ribozyme sequence (immediately downstream of the VSV (-) DNA), and a T7 RNA polymerase transcription termination site. A plasmid that can also be made and used is plasmid pVSVSS1, a portion of the sequence of which is shown in Fig. 2, in which a synthetic DNA polylinker, facilitating insertion of foreign DNA, has been inserted into pVSVFL(+) between the G and L coding regions. The polylinker was synthesized on a DNA synthesizer so as to have ends compatible for ligation into an NheI site, and to contain the unique restriction enzyme recognition sites XmaI, SmaI, and NotI, facilitating insertion of foreign DNA generated by cleavage with one of these enzymes or ligated to a linker containing a recognition site for one of these enzymes (which is then subjected to cleavage prior to insertion).

The foreign DNA encoding an Antigen is inserted into any region, or replaces any region, of the vesiculovirus (-) DNA that is not essential for vesiculovirus replication. In a preferred embodiment, the foreign DNA is thus inserted into an intergenic region, or a portion of the vesiculovirus (-) DNA that is transcribed to form the noncoding region of a viral mRNA. In a preferred embodiment,

the invention provides a nucleic acid comprising the DNA sequence of plasmid pVSVFL(+) as depicted in Figure 1 from nucleotide numbers 623-12088 (a portion of SEQ ID NO:1), in which a region nonessential for vesiculovirus replication has been inserted into or replaced by foreign DNA.

Vesiculoviruses have a defined intergenic structure. Extensive homologies are found around the intergenic dinucleotides (Fig. 3). These regions have the common structure (3')AUACUUUUUUUNAUUGUCNNUAG(5')

- 10 (SEQ ID NO:34), in which N indicates any nucleotide (thus three variable positions are present) and the intergenic dinucleotide is underlined. These dinucleotide spacers are GA, except at the NS-M junction, where the dinucleotide is CA. The first 11 nucleotides of the common sequence are
 15 complementary to the sequence (5') . . . UAUGAAAAAAA . . . (3') (SEQ ID NO:35) that occurs at the mRNA-polyadenylate[poly(A)] junction in each mRNA including L. Reiterative copying of the U residues by the VSV polymerase presumably generates the poly(A) tail on each mRNA
 20 (McGeoch, 1979, Cell 17:3199; Rose, 1980, Cell 19:415; Schubert et al., 1980, J. Virol. 34:550). The sequence complementary to the 5' end of the mRNA follows the intergenic dinucleotide. The L mRNA also terminates with the sequence UAUG-poly(A) encoded by the sequence (3')AUACUUUUUU
 25 (SEQ ID NO:36) and is presumably also polyadenylated by a polymerase "slippage" mechanism (Schubert et al., 1980, J. Virol. 34:550; Schubert and Lazarini, 1981, J. Virol. 38:256).

Thus, intergenic regions in vesiculovirus (-) DNA
 30 consist of three parts, triggering transcriptional termination and reinitiation present both 5' and 3' to each gene (presented as the 5' to 3' sequence of the positive sense strand of vesiculovirus (-) DNA): (a) TATGAAAAAAA (SEQ ID NO:37), followed by (b) the dinucleotide GT or CT,
 35 followed by (c) AACAG. Therefore, in a preferred aspect, foreign DNA encoding an Antigen can readily be expressed as a nonfusion protein from intergenic regions, simply by ensuring

that this three-part intergenic region is reconstituted -- i.e., that this intergenic region appears 5' and 3' to the foreign DNA and also 5' and 3' to the adjacent genes. For example, in a preferred embodiment, DNA consisting of (a) this three-part intergenic region, fused to (b) foreign DNA coding for a desired Antigen (preferably including the Antigen gene's native start and stop codons for initiation), is inserted into a portion of the vesiculovirus (-) DNA that is transcribed to form the 3' noncoding region of any vesiculovirus mRNA. In a particularly preferred aspect, the foreign DNA is inserted in the noncoding region between G and L.

In an alternative embodiment, the foreign DNA can be inserted into the G gene, so as to encode a fusion protein with G, for resultant surface display of the Antigen on the vesiculovirus particle. Selection should be undertaken to ensure that the foreign DNA insertion does not disrupt G protein function.

In a preferred embodiment, an Antigen expressed by a recombinant vesiculovirus is all or a portion of an envelope glycoprotein of a virus other than a vesiculovirus. Such an Antigen can replace the endogenous vesiculovirus G protein in the vesiculovirus, or can be expressed as a fusion with the endogenous G protein, or can be expressed in addition to the endogenous G protein either as a fusion or nonfusion protein. In a specific embodiment, such an Antigen forms a part of the vesiculovirus envelope and thus is surface-displayed in the vesiculovirus particle. By way of example, gp160 or a fragment thereof of Human Immunodeficiency Virus can be the Antigen, which is cleaved to produce gp120 and gp41 (see Owens and Rose, 1993, J. Virol. 67(1):360-365). In a specific embodiment, the G gene of VSV in the VSV (-) DNA of plasmid pVSVFL(+) can be easily excised and replaced, by cleavage at the NheI and MluI sites flanking the G gene and insertion of the desired sequence. In another specific embodiment, the Antigen is a foreign

envelope glycoprotein or portion thereof that is expressed as a fusion protein comprising the cytoplasmic domain (and, optionally, also the transmembrane region) of the native vesiculovirus G protein (see Owens and Rose, 1993, J. Virol. 5 67(1):360-365). Such a fusion protein can replace or be expressed in addition to the endogenous vesiculovirus G protein. As shown by way of example in Section 6 below, the entire native G coding sequence can be replaced by a coding sequence of a different G to produce recombinant replicable 10 vesiculoviruses that express a non-native glycoprotein.

While recombinant vesiculoviruses that express and display epitope(s) of envelope glycoproteins of other viruses can be used as live vaccines, such vesiculoviruses also are particularly useful as killed vaccines, as well as in the 15 production of subunit vaccines containing the vesiculovirus-produced protein comprising such epitope(s).

In a specific embodiment, a recombinant vesiculovirus of the invention expresses in a host to which it is administered one or more Antigens. In one embodiment, 20 a multiplicity of Antigens are expressed, each displaying different antigenicity or immunogenicity.

5.2. DNA SEQUENCES ENCODING ANTIGENS

The invention provides recombinant vesiculoviruses 25 capable of replication that have a foreign RNA sequence inserted into or replacing a site of the genome nonessential for replication, wherein the foreign RNA sequence (which is in the negative sense) directs the production of an Antigen capable of being expressed in a host infected by the 30 recombinant virus. This recombinant genome is originally produced by insertion of foreign DNA encoding the Antigen into the vesiculovirus (-) DNA. Any DNA sequence which encodes an immunogenic (capable of provoking an immune response) Antigen, which produces prophylactic or therapeutic 35 immunity against a disease or disorder, when expressed as a fusion or, preferably, nonfusion protein in a recombinant vesiculovirus of the invention, alone or in combination with

other Antigens expressed by the same or a different vesiculovirus recombinant, can be isolated for use in the vaccine formulations of the present invention.

In a preferred embodiment, expression of an Antigen
5 by a recombinant vesiculovirus induces an immune response against a pathogenic microorganism. For example, an Antigen may display the immunogenicity or antigenicity of an antigen found on bacteria, parasites, viruses, or fungi which are causative agents of diseases or disorders. In a preferred
10 embodiment, Antigens displaying the antigenicity or immunogenicity of antigens of animal viruses of veterinary importance (for example, which cause diseases or disorders in non-human animals such as domestic or farm animals, e.g., cows, chickens, horses, dogs, cats, etc.) are used. In
15 another embodiment, Antigens displaying the antigenicity or immunogenicity of an antigen of a human pathogen are used.

To determine immunogenicity or antigenicity by detecting binding to antibody, various immunoassays known in the art can be used, including but not limited to competitive
20 and non-competitive assay systems using techniques such as radioimmunoassays, ELISA (enzyme linked immunosorbent assay), "sandwich" immunoassays, immunoradiometric assays, gel diffusion precipitin reactions, immunodiffusion assays, in situ immunoassays (using colloidal gold, enzyme or
25 radioisotope labels, for example), western blots, immunoprecipitation reactions, agglutination assays (e.g., gel agglutination assays, hemagglutination assays), complement fixation assays, immunofluorescence assays, protein A assays, and immunoelectrophoresis assays, etc. In
30 one embodiment, antibody binding is detected by detecting a label on the primary antibody. In another embodiment, the primary antibody is detected by detecting binding of a secondary antibody or reagent to the primary antibody. In a further embodiment, the secondary antibody is labelled. Many
35 means are known in the art for detecting binding in an immunoassay and are envisioned for use. In one embodiment for detecting immunogenicity, T cell-mediated responses can

be assayed by standard methods, e.g., in vitro cytotoxicity assays or in vivo delayed-type hypersensitivity assays.

Parasites and bacteria expressing epitopes (antigenic determinants) that can be expressed by recombinant vesiculoviruses (wherein the foreign RNA directs the production of an antigen of the parasite or bacteria or a derivative thereof containing an epitope thereof) include but are not limited to those listed in Table II.

10

TABLE II

PARASITES AND BACTERIA EXPRESSING EPITOPES
THAT CAN BE EXPRESSED BY RECOMBINANT VESICULOVIRUSES

15

PARASITES:

Plasmodium spp.
Eimeria spp.

BACTERIA:

20

Vibrio cholerae
Streptococcus pneumoniae
Neisseria meningitidis
Neisseria gonorrhoeae
Corynebacteria diphtheriae
Clostridium tetani
Bordetella pertussis
Haemophilus spp. (e.g., *influenzae*)
Chlamydia spp.
Enterotoxigenic *Escherichia coli*

25

In another embodiment, the Antigen comprises an epitope of an antigen of a nematode, to protect against disorders caused by such worms.

30

In another specific embodiment, any DNA sequence which encodes a *Plasmodium* epitope, which when expressed by a recombinant vesiculovirus, is immunogenic in a vertebrate host, can be isolated for insertion into vesiculovirus (-) DNA according to the present invention. The species of *Plasmodium* which can serve as DNA sources include but are not limited to the human malaria parasites *P. falciparum*, *P.*

35

malariae, *P. ovale*, *P. vivax*, and the animal malaria parasites *P. berghei*, *P. yoelii*, *P. knowlesi*, and *P. cynomolgi*. In a particular embodiment, the epitope to be expressed is an epitope of the circumsporozoite (CS) protein of a species of *Plasmodium* (Miller et al., 1986, Science 234:1349).

In yet another embodiment, the Antigen comprises a peptide of the β subunit of Cholera toxin (Jacob et al., 1983, Proc. Natl. Acad. Sci. USA 80:7611).

10 Viruses expressing epitopes (antigenic determinants) that can be expressed by recombinant vesiculoviruses (wherein the foreign RNA directs the production of an antigen of the virus or a derivative thereof comprising an epitope thereof) include but are not limited to
15 those listed in Table III, which lists such viruses by family for purposes of convenience and not limitation (see 1990, Fields Virology, 2d ed., Fields and Knipe (eds.), Raven Press, NY).

20

TABLE III

VIRUSES EXPRESSING EPITOPES THAT CAN
BE EXPRESSED BY RECOMBINANT VESICULOVIRUSES

- | | | |
|----|------|--|
| 25 | I. | Picornaviridae |
| | | Enteroviruses |
| | | Poliovirus |
| | | Coxsackievirus |
| | | Echovirus |
| | | Rhinoviruses |
| | | Hepatitis A Virus |
| 30 | II. | Caliciviridae |
| | | Norwalk group of viruses |
| | III. | Togaviridae and Flaviviridae |
| | | Togaviruses (e.g., Dengue virus) |
| | | Alphaviruses |
| | | Flaviviruses (e.g., Hepatitis C virus) |
| | | Rubella virus |
| 35 | IV. | Coronaviridae |
| | | Coronaviruses |

- V. Rhabdoviridae
Rabies virus
- VI. Filoviridae
Marburg viruses
Ebola viruses
- 5 VII. Paramyxoviridae
Parainfluenza virus
Mumps virus
Measles virus
Respiratory syncytial virus
- 10 VIII. Orthomyxoviridae
Orthomyxoviruses (e.g., Influenza virus)
- IX. Bunyaviridae
Bunyaviruses
- X. Arenaviridae
Arenaviruses
- 15 XI. Reoviridae
Reoviruses
Rotaviruses
Orbiviruses
- XII. Retroviridae
20 Human T Cell Leukemia Virus type I
Human T Cell Leukemia Virus type II
Human Immunodeficiency Viruses (e.g.,
type I and type II)
Simian Immunodeficiency Virus
Lentiviruses
- XIII. Papoviridae
25 Polyomaviruses
Papillomaviruses
Adenoviruses
- XIV. Parvoviridae
Parvoviruses
- 30 XV. Herpesviridae
Herpes Simplex Viruses
Epstein-Barr virus
Cytomegalovirus
Varicella-Zoster virus
Human Herpesvirus-6
Cercopithecine Herpes Virus 1 (B virus)
- 35 XVI. Poxviridae
Poxviruses

XVIII. Hepadnaviridae
Hepatitis B virus

5 In specific embodiments, the Antigen encoded by the
foreign sequences that is expressed upon infection of a host
by the recombinant vesiculovirus, displays the antigenicity
or immunogenicity of an influenza virus hemagglutinin
(Genbank accession no. J02132; Air, 1981, Proc. Natl. Acad.
10 Sci. USA 78:7639-7643; Newton et al., 1983, Virology
128:495-501); human respiratory syncytial virus G
glycoprotein (Genbank accession no. Z33429; Garcia et al.,
1994, J. Virol.; Collins et al., 1984, Proc. Natl. Acad.
Sci. USA 81:7683); core protein, matrix protein or other
15 protein of Dengue virus (Genbank accession no. M19197; Hahn
et al., 1988, Virology 162:167-180), measles virus
hemagglutinin (Genbank accession no. M81899; Rota et al.,
1992, Virology 188:135-142); and herpes simplex virus type 2
glycoprotein gB (Genbank accession no. M14923; Bzik et al.,
20 1986, Virology 155:322-333).

In another embodiment, one or more epitopes of the
fusion protein of respiratory syncytial virus (RSV) can be
expressed as an Antigen.

Other Antigens that can be expressed by a
25 recombinant vesiculovirus include but are not limited to
those displaying the antigenicity or immunogenicity of the
following antigens: Poliovirus I VP1 (Emini et al., 1983,
Nature 304:699); envelope glycoproteins of HIV I (Putney et
al., 1986, Science 234:1392-1395); Hepatitis B surface
30 antigen (Itoh et al., 1986, Nature 308:19; Neurath et al.,
1986, Vaccine 4:34); Diphtheria toxin (Audibert et al., 1981,
Nature 289:543); streptococcus 24M epitope (Beachey, 1985,
Adv. Exp. Med. Biol. 185:193); and gonococcal pilin (Rothbard
and Schoolnik, 1985, Adv. Exp. Med. Biol. 185:247).

35 In other embodiments, the Antigen expressed by the
recombinant vesiculovirus displays the antigenicity or

immunogenicity of pseudorabies virus g50 (gpD), pseudorabies virus II (gpB), pseudorabies virus gIII (gpC), pseudorabies virus glycoprotein H, pseudorabies virus glycoprotein E, transmissible gastroenteritis glycoprotein 195, transmissible
 5 gastroenteritis matrix protein, swine rotavirus glycoprotein 38, swine parvovirus capsid protein, *Serpulina* *hyodysenteriae* protective antigen, Bovine Viral Diarrhea glycoprotein 55, Newcastle Disease Virus hemagglutinin-neuraminidase, swine flu hemagglutinin, or swine flu
 10 neuraminidase.

In various embodiments, the Antigen expressed by the recombinant vesiculovirus displays the antigenicity or immunogenicity of an antigen derived from *Serpulina* *hyodysenteriae*, Foot and Mouth Disease Virus, Hog Colera
 15 Virus, swine influenza virus, African Swine Fever Virus, *Mycoplasma hyopneumoniae*, infectious bovine rhinotracheitis virus (e.g., infectious bovine rhinotracheitis virus glycoprotein E or glycoprotein G), or infectious laryngotracheitis virus (e.g., infectious laryngotracheitis
 20 virus glycoprotein G or glycoprotein I).

In another embodiment, the Antigen displays the antigenicity or immunogenicity of a glycoprotein of La Crosse Virus (Gonzales-Scarano et al., 1982, Virology 120:42), Neonatal Calf Diarrhea Virus (Matsuno and Inouye, 1983,
 25 Infection and Immunity 39:155), Venezuelan Equine Encephalomyelitis Virus (Mathews and Roehrig, 1982, J. Immunol. 129:2763), Punta Toro Virus (Dalrymple et al., 1981, in Replication of Negative Strand Viruses, Bishop and Compans (eds.), Elsevier, NY, p. 167), Murine Leukemia Virus (Steeves
 30 et al., 1974, J. Virol. 14:187), or Mouse Mammary Tumor Virus (Massey and Schochetman, 1981, Virology 115:20).

In another embodiment, the Antigen displays the antigenicity or immunogenicity of an antigen of a human pathogen, including but not limited to human herpesvirus,
 35 herpes simplex virus-1, herpes simplex virus-2, human cytomegalovirus, Epstein-Barr virus, Varicella-Zoster virus, human herpesvirus-6, human herpesvirus-7, human influenza

virus, human immunodeficiency virus, rabies virus, measles virus, hepatitis B virus, hepatitis C virus, *Plasmodium falciparum*, and *Bordetella pertussis*.

In a specific embodiment of the invention, a
5 recombinant vesiculovirus expresses hepatitis B virus core protein and/or hepatitis B virus surface antigen or a fragment or derivative thereof (see, e.g., U.K. Patent Publication No. GB 2034323A published June 4, 1980; Ganem and Varmus, 1987, Ann. Rev. Biochem. 56:651-693; Tiollais et al.,
10 1985, Nature 317:489-495). The HBV genome (subtype adw) is contained in plasmid pAM6 (Moriarty et al., 1981, Proc. Natl. Acad. Sci. USA 78:2606-2610, available from the American Type Culture Collection (ATCC), Accession No. 45020), a
pBR322-based vector that is replicable in *E. coli*.

15 In another embodiment, the Antigen expressed by the recombinant vesiculovirus displays the antigenicity or immunogenicity of an antigen of equine influenza virus or equine herpesvirus. Examples of such antigens are equine influenza virus type A/Alaska 91 neuraminidase, equine
20 influenza virus type A/Miami 63 neuraminidase, equine influenza virus type A/Kentucky 81 neuraminidase equine herpesvirus type 1 glycoprotein B, and equine herpesvirus type 1 glycoprotein D.

In another embodiment, the Antigen displays the
25 antigenicity or immunogenicity of an antigen of bovine respiratory syncytial virus or bovine parainfluenza virus. For example, such antigens include but are not limited to bovine respiratory syncytial virus attachment protein (BRSV G), bovine respiratory syncytial virus fusion protein
30 (BRSV F), bovine respiratory syncytial virus nucleocapsid protein (BRSV N), bovine parainfluenza virus type 3 fusion protein, and the bovine parainfluenza virus type 3 hemagglutinin neuraminidase.

In another embodiment, the Antigen displays the
35 antigenicity or immunogenicity of bovine viral diarrhea virus glycoprotein 48 or glycoprotein 53.

In another embodiment, the Antigen displays the antigenicity or immunogenicity of an antigen of infectious bursal disease virus. Examples of such antigens are infectious bursal disease virus polyprotein and VP2.

- 5 Potentially useful antigens or derivatives thereof for use as Antigens expressed by recombinant vesiculoviruses can be identified by various criteria, such as the antigen's involvement in neutralization of a pathogen's infectivity (Norrby, 1985, Summary, in Vaccines85, Lerner et al. (eds.),
10 Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, pp. 388-389), type or group specificity, recognition by patients' antisera or immune cells, and/or the demonstration of protective effects of antisera or immune cells specific for the antigen. In addition, the antigen's encoded epitope
15 should preferably display a small or no degree of antigenic variation in time or amongst different isolates of the same pathogen.

- In a preferred embodiment, the foreign DNA inserted into the vesiculovirus (-) DNA encodes an ~~immunopotent~~
20 dominant epitope of a pathogen. Foreign DNA encoding epitopes which are reactive with antibody although incapable of eliciting immune responses, still have potential uses in immunoassays (see Section 5.8, *infra*).

- In another embodiment, foreign RNA of the
25 recombinant vesiculovirus directs the production of an Antigen comprising an epitope, which when the recombinant vesiculovirus is introduced into a desired host, induces an immune response that protects against a condition or disorder caused by an entity containing the epitope. For example, the
30 Antigen can be a tumor specific antigen or tumor-associated antigen, for induction of a protective immune response against a tumor (e.g., a malignant tumor). Such tumor-specific or tumor-associated antigens include but are not limited to KS 1/4 pan-carcinoma antigen (Perez and Walker,
35 1990, J. Immunol. 142:3662-3667; Bumal, 1988, Hybridoma 7(4):407-415); ovarian carcinoma antigen (CA125) (Yu et al., 1991, Cancer Res. 51(2):468-475); prostatic acid phosphate

(Tailor et al., 1990, Nucl. Acids Res. 18(16):4928); prostate specific antigen (Henttu and Vihko, 1989, Biochem. Biophys. Res. Comm. 160(2):903-910; Israeli et al., 1993, Cancer Res. 53:227-230; melanoma-associated antigen p97 (Estin et al., 5 1989, J. Natl. Cancer Instit. 81(6):445-446); melanoma antigen gp75 (Vijayasardahl et al., 1990, J. Exp. Med. 171(4):1375-1380); high molecular weight melanoma antigen (Natali et al., 1987, Cancer 59:55-63); and prostate specific membrane antigen.

10 In another embodiment of the invention, the Antigen expressed by the recombinant vesiculovirus comprises large regions of proteins which contain several B cell epitopes (i.e., epitopes capable of enticing a humoral immune response) and T cell epitopes (i.e., epitopes capable of 15 inducing a cell-mediated immune response).

Peptides or proteins which are known to contain antigenic determinants can be used as the Antigen. If specific desired antigens are unknown, identification and characterization of immunoreactive sequences can be carried 20 out. One way in which to accomplish this is through the use of monoclonal antibodies generated to the surface or other molecules of a pathogen or tumor, as the case may be. The peptide sequences capable of being recognized by the antibodies are defined epitopes. Alternatively, small 25 synthetic peptides conjugated to carrier molecules can be tested for generation of monoclonal antibodies that bind to the sites corresponding to the peptide, on the intact molecule (see, e.g., Wilson et al., 1984, Cell 37:767).

In a specific embodiment, appropriate Antigens, 30 including fragments or derivatives of known antigens, can be identified by virtue of their hydrophilicity, by carrying out a hydrophilicity analysis (Hopp and Woods, 1981, Proc. Natl. Acad. Sci. USA 78:3824) to generate a hydrophilicity profile. A hydrophilicity profile can be used to identify the 35 hydrophobic and hydrophilic regions of a protein and the corresponding regions of the gene sequence which encode such proteins. Hydrophilic regions are predicted to be

immunogenic/antigenic. Other methods known in the art which may be employed for the identification and characterization of antigenic determinants are also within the scope of the invention.

5 The foreign DNA encoding the Antigen, that is inserted into a non-essential site of the vesiculovirus (-) DNA, optionally can further comprise a foreign DNA sequence encoding a cytokine capable of being expressed and stimulating an immune response in a host infected by the
10 recombinant vesiculovirus. For example, such cytokines include but are not limited to interleukin-2, interleukin-6, interleukin-12, interferons, granulocyte-macrophage colony stimulating factors, and interleukin receptors.

 The foreign DNA optionally can further comprise a
15 sequence encoding and capable of expressing a detectable marker (e.g., β galactosidase).

5.3. CONSTRUCTION OF VESICULOVIRUS (-) DNA CONTAINING FOREIGN DNA

20 For initial production of a recombinant vesiculovirus, the foreign DNA comprising a sequence encoding the desired antigen is inserted into and/or replaces a region of the vesiculovirus (-) DNA nonessential for replication. Many strategies known in the art can be used in the
25 construction of the vesiculovirus (-) DNA containing the foreign DNA. For example, the relevant sequences of the foreign DNA and of the vesiculovirus (-) DNA can, by techniques known in the art, be cleaved at appropriate sites with restriction endonuclease(s), isolated, and ligated in
30 vitro. If cohesive termini are generated by restriction endonuclease digestion, no further modification of DNA before ligation may be needed. If, however, cohesive termini of the DNA are not available for generation by restriction endonuclease digestion, or different sites other than those
35 available are preferred, any of numerous techniques known in the art may be used to accomplish ligation of the heterologous DNA at the desired sites. In a preferred

embodiment, a desired restriction enzyme site is readily introduced into the desired DNA by amplification of the DNA by use of PCR with primers containing the restriction enzyme site. By way of another example, cleavage with a restriction enzyme can be followed by modification to create blunt ends by digesting back or filling in single-stranded DNA termini before ligation. Alternatively, the cleaved ends of the vesiculovirus (-) DNA or foreign DNA can be "chewed back" using a nuclease such as nuclease Bal 31, exonuclease III, lambda exonuclease, mung bean nuclease, or T4 DNA polymerase exonuclease activity, to name but a few, in order to remove portions of the sequence.

To facilitate insertion of the foreign DNA, an oligonucleotide sequence (a linker) which encodes one or more restriction sites can be inserted in a region of the vesiculovirus (-) DNA (see, e.g., the polylinker in pVSVSS1, Fig. 2) by ligation to DNA termini. A linker may also be used to generate suitable restriction sites in the foreign DNA sequence.

Additionally, vesiculovirus (-) DNA or foreign DNA sequences can be mutated *in vitro* or *in vivo* in order to form new restriction endonuclease sites or destroy preexisting ones, to facilitate *in vitro* ligation procedures. Any technique for mutagenesis known in the art can be used, including but not limited to, *in vitro* site-directed mutagenesis (Hutchinson et al., 1978, J. Biol. Chem. 253:6551), chemical mutagenesis, etc.

Sequences of the vesiculovirus (-) DNA that have been undesirably modified by such *in vitro* manipulations can be "restored," if desired, by introduction of appropriate sequences at the desired sites.

The particular strategy for inserting the foreign DNA will depend on the specific vesiculovirus (-) DNA site to be replaced or inserted into, as well as the foreign DNA to be inserted.

The sequences encoding the immunogenic peptides or proteins are preferably present in single copies, but can also be present in multiple copies within the virus genome.

Formation of the desired vesiculovirus (-) DNA 5 containing the foreign DNA can be confirmed by standard methods such as DNA sequence analysis, hybridization analysis, and/or restriction mapping, using methods well known in the art.

Foreign DNA encoding a desired antigen can be 10 obtained from any of numerous sources such as cloned DNA, genomic DNA, or cDNA made from RNA of the desired pathogen or tumor, as the case may be, or chemically synthesized DNA, and manipulated by recombinant DNA methodology well known in the art (see Sambrook et al., 1991, Molecular Cloning, A 15 Laboratory Manual, 2d ed., Cold Spring Harbor Laboratory Press, New York). In a preferred embodiment, polymerase chain reaction (PCR) is used to amplify the desired fragment of foreign DNA from among a crude preparation of DNA or a small sample of the DNA, by standard methods. Appropriate 20 primers for use in PCR can be readily deduced based on published sequences.

In order to generate appropriate DNA fragments, the DNA (e.g., from the pathogen or tumor of interest) may be cleaved at specific sites using various restriction enzymes. 25 Alternatively, one may use DNaseI in the presence of manganese, or mung bean nuclease (McCutchan et al., 1984, Science 225:626), to fragment the DNA, or the DNA can be physically sheared, as for example, by sonication. The linear DNA fragments can then be separated according to size 30 by standard techniques, including, but not limited to, agarose and polyacrylamide gel electrophoresis and column chromatography.

PCR amplification of DNA fragments containing the desired epitope(s) is most preferably carried out, in which 35 the PCR primers contain and thus introduce into the amplified DNA a desired restriction enzyme recognition site. Alternatively, any restriction enzyme or combination of

restriction enzymes may be used to generate DNA fragment(s) containing the desired epitope(s), provided the enzymes do not destroy the immunopotency of the encoded product.

Consequently, many restriction enzyme combinations may be used to generate DNA fragments which, when inserted into the vesiculovirus (-) DNA, are capable of producing recombinant vesiculoviruses that direct the production of the peptide containing the epitope(s).

Once the DNA fragments are generated, identification of the specific fragment containing the desired sequence may be accomplished in a number of ways. For example, if a small amount of the desired DNA sequence or a homologous sequence is previously available, it can be used as a labeled probe (e.g., nick translated) to detect the DNA fragment containing the desired sequence, by nucleic acid hybridization. Alternatively, if the sequence of the derived gene or gene fragment is known, isolated fragments or portions thereof can be sequenced by methods known in the art, and identified by a comparison of the derived sequence to that of the known DNA or protein sequence. Alternatively, the desired fragment can be identified by techniques including but not limited to mRNA selection, making cDNA to the identified mRNA, chemically synthesizing the gene sequence (provided the sequence is known), or selection on the basis of expression of the encoded protein (e.g., by antibody binding) after "shotgun cloning" of various DNA fragments into an expression system.

The sequences encoding peptides to be expressed in recombinant vesiculoviruses according to the present invention, whether produced by recombinant DNA methods, chemical synthesis, or purification techniques, include but are not limited to sequences encoding all or part (fragments) of the amino acid sequences of pathogen-specific and tumor-specific antigens, as well as other derivatives and analogs thereof displaying the antigenicity or immunogenicity thereof. Derivatives or analogs of antigens can be tested

for the desired activity by procedures known in the art, including but not limited to standard immunoassays.

In particular, antigen derivatives can be made by altering the encoding antigen nucleotide sequences by
5 substitutions, additions or deletions that do not destroy the antigenicity or immunogenicity of the antigen. For example, due to the degeneracy of nucleotide coding sequences, other DNA sequences which encode substantially the same amino acid sequence as a native antigen gene or portion thereof may be
10 used in the practice of the present invention. Other examples may include but are not limited to nucleotide sequences comprising all or portions of genes or cDNAs which are altered by the substitution of different codons that encode a functionally equivalent amino acid residue within
15 the sequence, thus producing a silent change. For example, one or more amino acid residues within the sequence can be substituted by another amino acid of a similar polarity which acts as a functional equivalent, resulting in a silent alteration. Substitutes for an amino acid within the
20 sequence may be selected from other members of the class to which the amino acid belongs. For example, the nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine. The polar neutral amino acids include glycine,
25 serine, threonine, cysteine, tyrosine, asparagine, and glutamine. The positively charged (basic) amino acids include arginine, lysine, and histidine. The negatively charged (acidic) amino acids include aspartic and glutamic acid.

30 The antigen derivatives and analogs can be produced by various methods known in the art. For example, a cloned gene sequence can be modified by any of numerous strategies known in the art (Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, 2d ed., Cold Spring Harbor Laboratory,
35 Cold Spring Harbor, New York). The sequence can be cleaved at appropriate sites with restriction endonuclease(s), followed by further enzymatic modification if desired,

isolated, and ligated *in vitro*. In the production of the gene encoding a derivative or analog of an antigen, care should be taken to ensure that the modified gene remains within the same translational reading frame as the antigen, 5 uninterrupted by translational stop signals, in the gene region where the desired epitope(s) are encoded.

Additionally, the antigen-encoding nucleic acid sequence can be mutated *in vitro* or *in vivo*, to create and/or destroy translation, initiation, and/or termination 10 sequences, or to create variations in coding regions and/or form new restriction endonuclease sites or destroy preexisting ones, to facilitate further *in vitro* modification. Any technique for mutagenesis known in the art can be used, including but not limited to, *in vitro* site- 15 directed mutagenesis (Hutchinson, C., et al., 1978, J. Biol. Chem 253:6551), use of TAB® linkers (Pharmacia), etc.

In another specific embodiment, the encoded antigen derivative is a chimeric, or fusion, protein comprising a first protein or fragment thereof fused to a second, 20 different amino acid sequence. Such a chimeric protein is encoded by a chimeric nucleic acid in which the two coding sequences are joined inframe. Such a chimeric product can be made by ligating the appropriate nucleic acid sequences encoding the desired amino acid sequences to each other by 25 methods known in the art, in the proper coding frame. In a specific embodiment, a fusion protein is produced in which the first protein sequence contains an epitope of an antigen, and the second protein sequence contains an epitope of a different antigen.

30 Derivatives and fragments of known antigens can be readily tested by standard immunoassay techniques to ascertain if they display the desired immunogenicity or antigenicity, rendering a DNA sequence encoding such a fragment or derivative suitable for insertion into the 35 vesiculovirus (-) DNA.

A DNA sequence encoding an epitope that is a hapten, i.e., a molecule that is antigenic in that it can

react selectively with cognate antibodies, but not immunogenic in that it cannot elicit an immune response when administered without adjuvants or carrier proteins, can also be isolated for use, since it is envisioned that, in particular embodiments, presentation by the vesiculoviruses of the invention can confer immunogenicity to the hapten expressed by the virus.

Once identified and isolated, the foreign DNA containing the sequence(s) of interest is then inserted into the vesiculovirus (-) DNA, for production of a recombinant vesiculovirus.

5.4. PRODUCTION OF RECOMBINANT VESICULOVIRUSES

The recombinant vesiculoviruses of the invention are produced by providing in an appropriate host cell: vesiculovirus (-) DNA, in which regions nonessential for replication have been inserted into or replaced by foreign DNA comprising a sequence encoding an Antigen, and recombinant sources of vesiculovirus N protein, P protein, and L protein. The production is preferably *in vitro*, in cell culture.

The host cell used for recombinant vesiculovirus production can be any cell in which vesiculoviruses grow, e.g., mammalian cells and some insect (e.g., *Drosophila*) cells. Primary cells, or more preferably, cell lines can be used. A vast number of cell lines commonly known in the art are available for use. By way of example, such cell lines include but are not limited to BHK (baby hamster kidney) cells, CHO (Chinese hamster ovary) cells, HeLA (human) cells, mouse L cells, Vero (monkey) cells, ESK-4, PK-15, EMSK cells, MDCK (Madin-Darby canine kidney) cells, MDBK (Madin-Darby bovine kidney) cells, 293 (human) cells, and Hep-2 cells.

The sources of N, P, and L proteins can be the same or different recombinant nucleic acid(s), encoding and capable of expressing the N, P and L proteins in the host cell in which it is desired to produce recombinant vesiculovirus.

The nucleic acids encoding the N, P and L proteins are obtained by any means available in the art. The N, P and L nucleic acid sequences have been disclosed and can be used. For example, see Genbank accession no. J02428; Rose and Schubert, 1987, in *The Viruses: The Rhabdoviruses*, Plenum Press, NY, pp. 129-166. The sequences encoding the N, P and L genes can also be obtained from plasmid pVSVFL(+), deposited with the ATCC and assigned accession no. 97134, e.g., by PCR amplification of the desired gene (PCR; U.S. Patent Nos. 4,683,202, 4,683,195 and 4,889,818; Gyllenstein et al., 1988, Proc. Natl. Acad. Sci. USA 85:7652-7656; Ochman et al., 1988, Genetics 120:621-623; Loh et al., 1989, Science 243:217-220). If a nucleic acid clone of any of the N, P or L genes is not already available, the clone can be obtained by use of standard recombinant DNA methodology. For example, the DNA may be obtained by standard procedures known in the art by purification of RNA from vesiculoviruses followed by reverse transcription and polymerase chain reaction (Mullis and Faloona, 1987, Methods in Enzymology 155:335-350). Alternatives to isolating an N, P or L gene include, but are not limited to, chemically synthesizing the gene sequence itself. Other methods are possible and within the scope of the invention.

If desired, the identified and isolated gene can then optimally be inserted into an appropriate cloning vector prior to transfer to an expression vector.

Nucleic acids that encode derivatives (including fragments) and analogs of native N, P and L genes, as well as derivatives and analogs of the vesiculovirus (-) DNA can also be used in the present invention, as long as such derivatives and analogs retain function, as exemplified by the ability when used according to the invention to produce a replicable vesiculovirus containing a genomic RNA containing foreign RNA. In particular, derivatives can be made by altering sequences by substitutions, additions, or deletions that provide for functionally active molecules. Furthermore, due to the inherent degeneracy of nucleotide coding sequences,

other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be used in the practice of the methods of the invention. Amino acid substitutions may be made on the basis of similarity in
5 polarity, charge, solubility, hydrophobicity, hydrophilicity and/or the amphipathic nature of the residues involved.

The desired N/P/L-encoding nucleic acid is then preferably inserted into an appropriate expression vector, i.e., a vector which contains the necessary elements for the
10 transcription and translation of the inserted protein-coding sequence in the host in which it is desired to produce recombinant vesiculovirus, to create a vector that functions to direct the synthesis of the N/P/L protein that will subsequently assemble with the vesiculovirus genomic RNA
15 containing the foreign sequence (produced in the host cell from antigenomic vesiculovirus (+) RNA produced by transcription of the vesiculovirus (-) DNA). A variety of vector systems may be utilized to express the N, P and L-encoding sequences, as well as to transcribe the
20 vesiculovirus (-) DNA containing the foreign DNA, as long as the vector is functional in the host and compatible with any other vector present. Such vectors include but are not limited to bacteriophages, plasmids, or cosmids. In a preferred aspect, a plasmid expression vector is used. The
25 expression elements of vectors vary in their strengths and specificities. Any one of a number of suitable transcription and translation elements may be used, as long as they are functional in the host.

Standard recombinant DNA methods may be used to
30 construct expression vectors containing DNA encoding the N, P, and L proteins, and the vesiculovirus (-) DNA containing the foreign DNA, comprising appropriate transcriptional/translational control signals (see, e.g., Sambrook et al., 1989, *supra*, and methods described hereinabove).
35 (Translational control signals are not needed for transcription of the vesiculovirus (-) DNA, and thus may be omitted from a vector containing the vesiculovirus (-) DNA,

although such signals may be present in the vector and operably linked to other sequences encoding a protein which it is desired to express). Expression may be controlled by any promoter/enhancer element known in the art. Promoters
5 which may be used to control expression can be constitutive or inducible. In a specific embodiment, the promoter is an RNA polymerase promoter.

Transcription termination signals (downstream of the gene), and selectable markers are preferably also
10 included in a plasmid expression vector. In addition to promoter sequences, expression vectors for the N, P, and L proteins preferably contain specific initiation signals for efficient translation of inserted N/P/L sequences, e.g., a ribosome binding site.

15 Specific initiation signals are required for efficient translation of inserted protein coding sequences. These signals include the ATG initiation codon and adjacent sequences. In cases where the entire N, P, or L gene including its own initiation codon and adjacent sequences are
20 inserted into the appropriate vectors, no additional translational control signals may be needed. However, in cases where only a portion of the gene sequence is inserted, exogenous translational control signals, including the ATG initiation codon, must be provided. The initiation codon
25 must furthermore be in phase with the reading frame of the protein coding sequences to ensure translation of the entire insert. These exogenous translational control signals and initiation codons can be of a variety of origins, both natural and synthetic.

30 In a specific embodiment, a recombinant expression vector provided by the invention, encoding an N, P, and/or L protein or functional derivative thereof, comprises the following operatively linked components: a promoter which controls the expression of the N, P, or L protein or
35 functional derivative thereof, a translation initiation signal, a DNA sequence encoding the N, P or L protein or functional derivative thereof, and a transcription

termination signal. In a preferred aspect, the above components are present in 5' to 3' order as listed above.

In another specific embodiment, the gene encoding the N, P, or L protein is inserted downstream of the T7 RNA polymerase promoter from phage T7 gene 10, situated with an A in the -3 position. A T7 RNA polymerase terminator and a replicon are also included in the expression vector. In this embodiment, T7 RNA polymerase is provided to transcribe the N/P/L sequence. The T7 RNA polymerase can be produced from a chromosomally integrated sequence or episomally, and is most preferably provided by intracellular expression from a recombinant vaccinia virus encoding the T7 RNA polymerase (see *infra*). Preferably, the N, P, and L proteins are each encoded by a DNA sequence operably linked to a promoter in an expression plasmid, containing the necessary regulatory signals for transcription and translation of the N, P, and L proteins. Such an expression plasmid preferably includes a promoter, the coding sequence, and a transcription termination/polyadenylation signal, and optionally, a selectable marker (e.g., β -galactosidase). The N, P and L proteins can be encoded by the same or different plasmids, or a combination thereof, and preferably are in different plasmids. Less preferably, one or more of the N, P, and L proteins can be expressed intrachromosomally.

The cloned sequences comprising the vesiculovirus (-) DNA containing the foreign DNA, and the cloned sequences comprising sequences encoding the N, P, and L proteins can be introduced into the desired host cell by any method known in the art, e.g., transfection, electroporation, infection (when the sequences are contained in, e.g., a viral vector), microinjection, etc.

In a preferred embodiment, DNA comprising vesiculovirus (-) DNA containing foreign DNA encoding an Antigen, operably linked to an RNA polymerase promoter (preferably a bacteriophage RNA polymerase promoter); DNA encoding N, operably linked to the same RNA polymerase promoter; DNA encoding P, operably linked to the same

polymerase promoter; and DNA encoding L, operably linked to the same polymerase promoter; are all introduced (preferably by transfection) into the same host cell, in which host cell the RNA polymerase has been cytoplasmically provided. The

5 RNA polymerase is cytoplasmically provided preferably by expression from a recombinant virus that replicates in the cytoplasm and expresses the RNA polymerase, most preferably a vaccinia virus (see the section hereinbelow), that has been introduced (e.g., by infection) into the same host cell.

10 Cytoplasmic provision of RNA polymerase is preferred, since this will result in cytoplasmic transcription and processing, of the VSV (-) DNA comprising the foreign DNA and of the N, P and L proteins, avoiding splicing machinery in the cell nucleus, and thus maximizing proper processing and production

15 of N, P and L proteins, and resulting assembly of the recombinant vesiculovirus. For example, vaccinia virus also cytoplasmically provides enzymes for processing (capping and polyadenylation) of mRNA, facilitating proper translation. In a most preferred aspect, T7 RNA polymerase promoters are

20 employed, and a cytoplasmic source of T7 RNA polymerase is provided by also introducing into the host cell a recombinant vaccinia virus encoding T7 RNA polymerase into the host cell. Such vaccinia viruses can be obtained by well known methods (see section 5.5, *infra*). In a preferred aspect, a

25 recombinant vaccinia virus such as vTF7-3 (Fuerst et al., 1986, Proc. Natl. Acad. Sci. U.S.A. 83:8122-8126) can be used. In a most preferred aspect, the DNA comprising vesiculovirus (-) DNA containing foreign DNA is plasmid pVSVSS1 in which foreign DNA has been inserted into the

30 polylinker region.

Alternatively, but less preferably, the RNA polymerase (e.g., T7 RNA polymerase) can be provided by use of a host cell that expresses T7 RNA polymerase from a chromosomally integrated sequence (e.g., originally inserted

35 into the chromosome by homologous recombination), preferably constitutively, or that expresses T7 RNA polymerase episomally, from a plasmid.

In another, less preferred, embodiment, the VSV (-) DNA encoding an Antigen, operably linked to a promoter, can be transfected into a host cell that stably recombinantly expresses the N, P, and L proteins from chromosomally integrated sequences.

The cells are cultured and recombinant vesiculovirus is recovered, by standard methods. For example, and not by limitation, after approximately 24 hours, cells and medium are collected, freeze-thawed, and the lysates clarified to yield virus preparations.

Alternatively, the cells and medium are collected and simply cleared of cells and debris by low-speed centrifugation.

Confirmation that the appropriate foreign sequence is present in the genome of the recombinant vesiculovirus and directs the production of the desired protein(s) in an infected cell, is then preferably carried out. Standard procedures known in the art can be used for this purpose. For example, genomic RNA is obtained from the vesiculovirus by SDS-phenol extraction from virus preparations, and can be subjected to reverse transcription (and PCR, if desired), followed by sequencing, Southern hybridization using a probe specific to the foreign DNA, or restriction enzyme mapping, etc. The virus can be used to infect host cells, which can then be assayed for expression of the desired protein by standard immunoassay techniques using an antibody to the protein, or by assays based on functional activity of the protein. Other techniques are known in the art and can be used.

The invention also provides kits for production of recombinant vesiculoviruses. In one embodiment, the kit comprises in one or more (and most preferably, in separate) containers: (a) a first recombinant DNA that can be transcribed in a suitable host cell to produce a vesiculovirus antigenomic (+) RNA in which a portion of the RNA nonessential for replication of the vesiculovirus has been inserted into or replaced by a foreign RNA sequence; (b) a second recombinant DNA comprising a sequence encoding a

vesiculovirus N protein; (c) a third recombinant DNA comprising a sequence encoding a vesiculovirus L protein; and (d) a fourth recombinant DNA comprising a sequence encoding a vesiculovirus P protein. The second, third and fourth
5 recombinant DNAs can be part of the same or different DNA molecules. In a preferred embodiment, the sequences encoding the N, L, and P proteins are each operably linked to a promoter that controls expression of the N, L, and P proteins, respectively, in the suitable host cell. In
10 various embodiments, the kit can contain the various nucleic acids, e.g., plasmid expression vectors, described hereinabove for use in production of recombinant vesiculoviruses.

In another embodiment, a kit of the invention
15 comprises (a) a first recombinant DNA that can be transcribed in a suitable host cell to produce a vesiculovirus antigenomic DNA in which a portion of the RNA nonessential for replication of the vesiculovirus has been inserted into or replaced by a foreign RNA sequence; and (b) a host cell
20 that recombinantly expresses vesiculovirus N, P and L proteins.

In a preferred embodiment, a kit of the invention comprises in separate containers:

(a) a first plasmid comprising the following
25 operatively linked components: (i) a bacteriophage RNA polymerase promoter, (ii) a DNA comprising a sequence capable of being transcribed in a suitable host cell to produce an RNA molecule comprising a vesiculovirus antigenomic RNA in which a portion of the RNA nonessential for replication of
30 the vesiculovirus has been inserted into or replaced by a foreign RNA sequence, and in which the 3' end of the antigenomic RNA is immediately adjacent to a ribozyme sequence that cleaves at the 3' end of the antigenomic RNA, and (iii) a transcriptional termination signal for the
35 bacteriophage RNA polymerase; and

(b) a second plasmid comprising the following operatively linked components: (i) the bacteriophage RNA

polymerase promoter, (ii) a DNA comprising a sequence encoding the vesiculovirus N protein, and (ii) a transcriptional termination signal for the bacteriophage RNA polymerase; and

5 (c) a third plasmid comprising the following operatively linked components: (i) the bacteriophage RNA polymerase promoter, (ii) a DNA comprising a sequence encoding the vesiculovirus P protein, and (ii) a transcriptional termination signal for the bacteriophage RNA
10 polymerase; and

(d) a fourth plasmid comprising the following operatively linked components: (i) the bacteriophage RNA polymerase promoter, (ii) a DNA comprising a sequence encoding the vesiculovirus L protein, and (ii) a
15 transcriptional termination signal for the bacteriophage RNA polymerase.

In another embodiment, a kit of the invention further comprises in a separate container a recombinant vaccinia virus encoding and capable of expressing the
20 bacteriophage RNA polymerase.

In a preferred embodiment, the components in the containers are in purified form.

25 5.4.1. RECOMBINANT VACCINIA VIRUSES
ENCODING AND CAPABLE OF
EXPRESSING FOREIGN RNA POLYMERASES

In a preferred aspect of the invention, transcription of the vesiculovirus (-) DNA containing the foreign DNA encoding an Antigen, and/or transcription of the DNA encoding the N, P, and L proteins in the host cell, is
30 controlled by an RNA polymerase promoter (preferably one in which the RNA polymerase is not endogenous to the host cell), and the RNA polymerase (that initiates transcription from the promoter) is recombinantly provided in the host cell by
expression from a recombinant vaccinia virus. DNA sequences
35 encoding RNA polymerases are well known and available in the

art and can be used. For example, phage DNA can be obtained and PCR used to amplify the desired polymerase gene.

Insertion of the desired recombinant DNA sequence encoding and capable of expressing the RNA polymerase into a
5 vaccinia virus for expression by the vaccinia virus is preferably accomplished by first inserting the DNA sequence into a plasmid vector which is capable of subsequent transfer to a vaccinia virus genome by homologous recombination. Thus, in a preferred aspect of the invention for constructing
10 the recombinant vaccinia viruses, the desired DNA sequence encoding the polymerase is inserted, using recombinant DNA methodology (see Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, 2d ed., Cold Spring Harbor Laboratory, Cold Spring Harbor, New York) into an insertion (preferably,
15 plasmid) vector flanked by (preferably) nonessential vaccinia DNA sequences, thus providing for subsequent transfer of its chimeric gene(s) into vaccinia virus by homologous recombination. The sequences are placed in the vector such that they can be expressed under the control of a promoter
20 functional in vaccinia virus.

Expression of foreign DNA in recombinant vaccinia viruses requires the positioning of promoters functional in vaccinia so as to direct the expression of the protein-coding polymerase DNA sequences. Plasmid insertion vectors have
25 been constructed to insert chimeric genes into vaccinia virus for expression therein. Examples of such vectors are described by Mackett (Mackett et al., 1984. J. Virol. 49:857-864). The DNA encoding the polymerase is inserted into a suitable restriction endonuclease cloning site. In addition
30 to plasmid insertion vectors, insertion vectors based on single-stranded M13 bacteriophage DNA (Wilson et al., 1986, Gene 49:207-213) can be used.

The inserted polymerase DNA should preferably not contain introns, and insertion should preferably be so as to
35 place the coding sequences in close proximity to the promoter, with no other start codons in between the initiator ATG and the 5' end of the transcript.

The plasmid insertion vector should contain transcriptional and translational regulatory elements that are active in vaccinia virus. The plasmid should be configured so that the polymerase sequences are under the control of a promoter active in vaccinia virus. Promoters which can be used in the insertion vectors include but are not limited to the vaccinia virus thymidine kinase (TK) promoter, the 7.5K promoter (Cochran et al., 1985, J. Virol. 54:30-37), the 11K promoter (European Patent Publication 0198328), the F promoter (Paoletti et al., 1984, Proc. Natl. Acad. Sci. USA 81:193-197), and various early and late vaccinia promoters (see Moss, 1990, Virology, 2d ed., ch. 74, Fields et al., eds., Raven Press, Ltd., New York, pp. 2079-2111).

In a specific embodiment, the plasmid insertion vector contains (for eventual transfer into vaccinia virus) a T7 RNA polymerase coding sequence under the control of a promoter active in vaccinia virus. In another specific embodiment, a plasmid insertion vector contains a co-expression system consisting of divergently oriented promoters, one directing transcription of the polymerase sequences, the other directing transcription of a reporter gene or selectable marker, to facilitate detection or selection of the eventual recombinant vaccinia virus (see, e.g., Fuerst et al., 1987, Mol. Cell. Biol. 5:1918-1924).

As described supra, the plasmid insertion vector contains at least one set of polymerase coding sequences operatively linked to a promoter, flanked by sequences preferably nonessential for vaccinia viral replication. Such nonessential sequences include but are not limited to the TK gene (Mackett et al., 1984, J. Virol. 49:857-864), the vaccinia HindIII-F DNA fragment (Paoletti et al., 1984, Proc. Natl. Acad. Sci. USA 81:193-197), the vaccinia growth factor gene situated within both terminal repeats (Buller et al., 1988, J. Virol. 62:866-874), the N2 and M1 genes (Tamin et al., 1988, Virology 165:141-150), the M1 subunit of the ribonucleotide reductase gene in the vaccinia HindIII-I DNA

fragment (Child et al., 1990, Virology 174:625-629), the vaccinia hemagglutinin (Shida et al., 1988, J. Virol. 62:4474-4480), vaccinia 14 kD fusion protein gene (Rodriguez et al., 1989, Proc. Natl. Acad. Sci. USA 86:1287-1291), etc. 5 (see also Buller and Palumbo, 1991, Microbiol. Rev. 55(1):80-122). TK sequences are preferred for use; use of such sequences results in the generation of TK⁻ recombinant viruses.

Recombinant vaccinia viruses are preferably 10 produced by transfection of the recombinant insertion vectors containing the polymerase sequences into cells previously infected with vaccinia virus. Alternatively, transfection can take place prior to infection with vaccinia virus. Homologous recombination takes place within the infected 15 cells and results in the insertion of the foreign gene into the viral genome, in the region corresponding to the insertion vector flanking regions. The infected cells can be screened using a variety of procedures such as immunological techniques, DNA plaque hybridization, or genetic selection 20 for recombinant viruses which subsequently can be isolated. These vaccinia recombinants preferably retain their essential functions and infectivity and can be constructed to accommodate up to approximately 35 kilobases of foreign DNA.

Transfections may be performed by procedures known 25 in the art, for example, a calcium chloride-mediated procedure (Mackett et al., 1985, The construction and characterization of vaccinia virus recombinants expressing foreign genes, in *DNA Cloning*, Vol. II, Rickwood and Hames (eds.), IRL Press, Oxford-Washington, D.C.) or a 30 liposome-mediated procedure (Rose et al., 1991, Biotechniques 10:520-525).

Where, as is preferred, flanking TK sequences are used to promote homologous recombination, the resulting recombinant viruses thus have a disrupted TK region, 35 permitting them to grow on a TK⁻ host cell line such as Rat2 (ATCC Accession No. CRL 1764) in the presence of

identity and purity, and expression of the inserted polymerase.

5.5. LARGE SCALE GROWTH AND PURIFICATION
OF RECOMBINANT REPLICABLE VESICULOVIRUSES

5 The recovered recombinant vesiculovirus, after plaque-purification, can then be grown to large numbers, by way of example, as follows. Virus from a single plaque ($\sim 10^6$ pfu) is recovered and used to infect $\sim 10^7$ cells (e.g., BHK cells), to yield, typically, 10 ml at a titer of 10^9 - 10^{10} pfu/ml for a total of approximately 10^{11} pfu. Infection of $\sim 10^{12}$ cells can then be carried out (with a multiplicity of infection of 0.1), and the cells can be grown in suspension culture, large dishes, or roller bottles by standard methods.

15 It is noted that recombinant vesiculoviruses which no longer express the extracellular region of the vesiculovirus G protein (which determine host range) and which, instead, express an envelope glycoprotein of a different virus will need to be grown in cells which are susceptible to infection by the different virus (and which cells thus express a receptor promoting infection by a virus expressing the envelope glycoprotein of the different virus). Thus, for example, where the recombinant vesiculovirus expresses the HIV envelope glycoprotein, the virus is grown in $CD4^+$ cells (e.g., $CD4^+$ lymphoid cells).

25 Virus for vaccine preparations can then be collected from culture supernatants, and the supernatants clarified to remove cellular debris. If desired, one method of isolating and concentrating the virus that can be employed is by passage of the supernatant through a tangential flow membrane concentration. The harvest can be further reduced in volume by pelleting through a glycerol cushion and by concentration on a sucrose step gradient. An alternate method of concentration is affinity column purification (Daniel et al., 1988, Int. J. Cancer 41:601-608). However, other methods can also be used for purification (see, e.g., Arthur et al., 1986, J. Cell. Biochem. Suppl. 10A:226), and

any possible modifications of the above procedure will be readily recognized by one skilled in the art. Purification should be as gentle as possible, so as to maintain the integrity of the virus particle.

5

5.6. RECOMBINANT REPLICABLE VESICULOVIRUSES
FOR USE AS LIVE VACCINES

In one embodiment of the invention, the recombinant replicable vesiculoviruses that express an immunogenic
10 Antigen are used as live vaccines.

The recombinant vesiculoviruses for use as therapeutic or prophylactic live vaccines according to the invention are preferably somewhat attenuated. Most available strains e.g., laboratory strains of VSV, may be sufficiently
15 attenuated for use. Should additional attenuation be desired, e.g., based on pathogenicity testing in animals, attenuation is most preferably achieved simply by laboratory passage of the recombinant vesiculovirus (e.g., in BHK or any other suitable cell line). Generally, attenuated viruses are
20 obtainable by numerous methods known in the art including but not limited to chemical mutagenesis, genetic insertion, deletion (Miller, 1972, Experiments in Molecular Genetics, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY) or recombination using recombinant DNA methodology (Maniatis et
25 al., 1982, Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY), laboratory selection of natural mutants, etc.

In this embodiment of the invention, a vaccine is formulated in which the immunogen is one or several
30 recombinant vesiculovirus(es), in which the foreign RNA in the genome directs the production of an Antigen in a host so as to elicit an immune (humoral and/or cell mediated) response in the host that is prophylactic or therapeutic. In an embodiment wherein the Antigen displays the antigenicity
35 or immunogenicity of an antigen of a pathogen, administration of the vaccine is carried out to prevent or treat an infection by the pathogen and/or the resultant infectious

disorder and/or other undesirable correlates of infection. In an embodiment wherein the Antigen is a tumor antigen, administration of the vaccine is carried out to prevent or treat tumors (particularly, cancer).

5 In a preferred specific embodiment, the recombinant vesiculoviruses are administered prophylactically, to prevent/protect against infection and/or infectious diseases or tumor (e.g., cancer) formation.

In a specific embodiment directed to therapeutics, 10 the recombinant vesiculoviruses of the invention, encoding immunogenic epitope(s), are administered therapeutically, for the treatment of infection or tumor formation.

Administration of such viruses, e.g., to neonates and other human subjects, can be used as a method of immunostimulation, 15 to boost the host's immune system, enhancing cell-mediated and/or humoral immunity, and facilitating the clearance of infectious agents or tumors. The viruses of the invention can be administered alone or in combination with other therapies (examples of anti-viral therapies, including but 20 not limited to α -interferon and vidarabine phosphate; examples of tumor therapy including but not limited to radiation and cancer chemotherapy).

5.7. INACTIVATED RECOMBINANT VESICULOVIRUSES FOR VACCINE USE

25 In a specific embodiment, the recombinant replicable vesiculoviruses of the invention are inactivated (i.e., killed, rendered nonreplicable) prior to vaccine use, to provide a killed vaccine. Since the vesiculovirus 30 envelope is highly immunogenic, in an embodiment wherein one or more foreign proteins (e.g., an envelope glycoprotein of a virus other than a vesiculovirus) is incorporated into the vesiculovirus envelope, such a virus, even in killed form, can be effective to provide an immune response against said 35 foreign protein(s) in a host to which it is administered. In a specific embodiment, a multiplicity of Antigens, each displaying the immunogenicity or antigenicity of an envelope

glycoprotein of a different virus, are present in the recombinant vesiculovirus particle.

The inactivated recombinant viruses of the invention differ from defective interfering particles in that, prior to inactivation the virus is replicable (*i.e.*, it encodes all the vesiculovirus proteins necessary to enable it to replicate in an infected cell). Thus, since the virus is originally in a replicable state, it can be easily propagated and grown to large amounts prior to inactivation, to provide a large amount of killed virus for use in vaccines, or for purification of the expressed antigen for use in a subunit vaccine (see Section 5.8, *infra*).

Various methods are known in the art and can be used to inactivate the recombinant replicable vesiculoviruses of the invention, for use as killed vaccines. Such methods include but are not limited to inactivation by use of formalin, betapropiolactone, gamma irradiation, and psoralen plus ultraviolet light.

In a specific embodiment, recombinant vesiculovirus can be readily inactivated by resuspension of purified virions in a suitable concentration of formaldehyde. While 0.8 formaldehyde may be sufficient, verification of the optimum concentration of formaldehyde can be readily determined for a particular virus by titration of serial dilutions of formaldehyde with infectious virus to determine the inactivation curve of formalin for that virus. This technique has been described in detail by Salk and Gori, 1960, *Ann. N.Y. Acad. Sci.* 83:609-637). By extrapolation to zero, the concentration expected to inactivate the last infectious particle can be estimated. By utilizing a substantially higher concentration, *e.g.*, 4-fold greater than the estimated concentration, complete inactivation can be assured.

Although formalin inactivation alone has proven to be effective, it may be desirable, for safety and regulatory purposes, to kill the virus twice or more, using one or more of the numerous other methods currently known for virus

inactivation. Thus, although not essential, it is contemplated that the virus used in the final formulation will be often inactivated by a second agent after treatment with formalin.

5

5.8. USE OF RECOMBINANT REPLICABLE VESICULOVIRUSES IN THE PRODUCTION OF SUBUNIT VACCINES

Since the recombinant vesiculoviruses of the invention can be propagated and grown to large amounts, where
10 the recombinant vesiculoviruses express an Antigen, growth of such vesiculoviruses provides a method for large scale production and ready purification of the expressed Antigen, particularly when the Antigen is incorporated into the envelope of the recombinant vesiculovirus. In a specific
15 embodiment, the Antigen is all or a portion of an envelope glycoprotein of another virus, e.g., HIV gp160, expressed as a nonfusion protein, or expressed as a fusion to the cytoplasmic domain of a vesiculovirus G protein.

The Antigens thus produced and purified have use in
20 subunit vaccines.

The recombinant vesiculoviruses that express an Antigen can also be used to recombinantly produce the Antigen in infected cells *in vitro*, to provide a source of Antigen for use in immunoassays, e.g., to detect or measure in a
25 sample of body fluid from a vaccinated subject the presence of antibodies to the Antigen, and thus to diagnose infection or the presence of a tumor and/or monitor immune response of the subject subsequent to vaccination.

30

5.9. DETERMINATION OF VACCINE EFFICACY

Immunopotency of the one or more Antigen(s) in its live or inactivated vesiculovirus vaccine formulation, or in
is subunit vaccine formulation, can be determined by
monitoring the immune response of test animals following
35 immunization with the recombinant vesiculovirus(es)
expressing the Antigen(s) or with the subunit vaccine

containing the Antigen, by use of any immunoassay known in the art. Generation of a humoral (antibody) response and/or cell-mediated immunity, may be taken as an indication of an immune response. Test animals may include mice, hamsters, 5 dogs, cats, monkeys, rabbits, chimpanzees, etc., and eventually human subjects.

Methods of introduction of the vaccine may include oral, intracerebral, intradermal, intramuscular, intraperitoneal, intravenous, subcutaneous, intranasal or any 10 other standard routes of immunization. The immune response of the test subjects can be analyzed by various approaches such as: the reactivity of the resultant immune serum to the Antigen, as assayed by known techniques, e.g., enzyme linked immunosorbent assay (ELISA), immunoblots, 15 radioimmunoprecipitations, etc.; or, in the case where the Antigen displays the antigenicity or immunogenicity of a pathogen's antigen, by protection of immunized hosts from infection by the pathogen and/or attenuation of symptoms due to infection by the pathogen in immunized hosts; or, in the 20 case where the antigen displays the antigenicity or immunogenicity of a tumor antigen, by prevention of tumor formation or prevention of metastasis, or by regression, or by inhibition of tumor progression, in immunized hosts.

As one example of suitable animal testing of a live 25 vaccine, live vaccines of the invention may be tested in rabbits for the ability to induce an antibody response to the Antigens. Male specific-pathogen-free (SPF) young adult New Zealand White rabbits may be used. The test group of rabbits each receives approximately 5×10^8 pfu (plaque forming units) 30 of the vaccine. A control group of rabbits receives an injection in 1 mM Tris-HCl pH 9.0 of a non-recombinant vesiculovirus or of a recombinant vesiculovirus which does not express the same Antigen.

Blood samples may be drawn from the rabbits every 35 one or two weeks, and serum analyzed for antibodies to the Antigen(s). The presence of antibodies specific for the Antigen(s) may be assayed, e.g., using an ELISA.

Animals may also be used to test vaccine efficacy (e.g., challenge experiments). For example, in a specific embodiment regarding a live vaccine formulation, monkeys each receive intradermally approximately 5×10^8 pfu of recombinant vesiculovirus. A control monkey receives (control) non-recombinant virus intradermally. Blood is drawn weekly for 12 weeks, and serum is analyzed for antibodies to the Antigen(s).

10 5.10. VACCINE FORMULATION AND ADMINISTRATION

The vaccines of the invention may be multivalent or univalent. Multivalent vaccines are made from recombinant viruses that direct the expression of more than one Antigen, from the same or different recombinant viruses.

15 Many methods may be used to introduce the vaccine formulations of the invention; these include but are not limited to oral, intradermal, intramuscular, intraperitoneal, intravenous, subcutaneous, intranasal routes, and via scarification (scratching through the top layers of skin,
20 e.g., using a bifurcated needle).

The patient to which the vaccine is administered is preferably a mammal, most preferably a human, but can also be a non-human animal including but not limited to cows, horses, sheep, pigs, fowl (e.g., chickens), goats, cats, dogs,
25 hamsters, mice and rats. In the use of a live vesiculovirus vaccine, the patient can be any animal in which vesiculovirus replicates (for example, the above-listed animals).

The virus vaccine formulations of the invention comprise an effective immunizing amount of one or more
30 recombinant vesiculoviruses (live or inactivated, as the case may be) and a pharmaceutically acceptable carrier or excipient. Subunit vaccines comprise an effective immunizing amount of one or more Antigens and a pharmaceutically acceptable carrier or excipient. Pharmaceutically acceptable
35 carriers are well known in the art and include but are not limited to saline, buffered saline, dextrose, water, glycerol, sterile isotonic aqueous buffer, and combinations

thereof. One example of such an acceptable carrier is a physiologically balanced culture medium containing one or more stabilizing agents such as stabilized, hydrolyzed proteins, lactose, etc. The carrier is preferably sterile.

5 The formulation should suit the mode of administration.

The composition, if desired, can also contain minor amounts of wetting or emulsifying agents, or pH buffering agents. The composition can be a liquid solution, suspension, emulsion, tablet, pill, capsule, sustained

10 release formulation, or powder. Oral formulation can include standard carriers such as pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharine, cellulose, magnesium carbonate, etc.

Generally, the ingredients are supplied either

15 separately or mixed together in unit dosage form, for example, as a dry lyophilized powder or water free concentrate in a hermetically sealed container such as an ampoule or sachette indicating the quantity of active agent. Where the composition is administered by injection, an

20 ampoule of sterile diluent can be provided so that the ingredients may be mixed prior to administration.

In a specific embodiment, a lyophilized recombinant vesiculovirus of the invention is provided in a first container; a second container comprises diluent consisting of

25 an aqueous solution of 50% glycerin, 0.25% phenol, and an antiseptic (e.g., 0.005% brilliant green).

The precise dose of virus, or subunit vaccine, to be employed in the formulation will also depend on the route of administration, and the nature of the patient, and should

30 be decided according to the judgment of the practitioner and each patient's circumstances according to standard clinical techniques. An effective immunizing amount is that amount sufficient to produce an immune response to the Antigen in the host to which the recombinant vesiculovirus, or subunit

35 vaccine, is administered.

In a specific embodiment, an effective immunizing amount of a live recombinant vesiculovirus of the present

invention is within the range of 10^3 to 10^9 pfu/dose, more preferably 10^6 to 10^9 pfu/dose. Boosting is possible but not preferred. If boosting is desired, one optionally may boost with the Antigen in purified form rather than using a
5 recombinant vesiculovirus of the invention.

For inactivated recombinant vesiculovirus vaccines, the vaccine formulation comprises an effective immunizing amount of the inactivated virus, preferably in combination with an immunostimulant; and a pharmaceutically acceptable
10 carrier. As used in the present context, "immunostimulant" is intended to encompass any compound or composition which has the ability to enhance the activity of the immune system, whether it be a specific potentiating effect in combination with a specific antigen, or simply an independent effect upon
15 the activity of one or more elements of the immune response. Some of the more commonly utilized immunostimulant compounds in vaccine compositions are the adjuvants alum or muramyl dipeptide (MDP) and its analogues. Methods of utilizing these materials are known in the art, and it is well within
20 the ability of the skilled artisan to determine an optimum amount of stimulant for a given virus vaccine. It may also be desired to use more than one immunostimulant in a given formulation.

The exact amount of inactivated virus utilized in a
25 given preparation is not critical, provided that the minimum amount of virus necessary to provoke an immune response is given. A dosage range of as little as about 10 μ g, up to amount a milligram or more, is contemplated. As one example, in a specific embodiment, individual dosages may range from
30 about 50-650 μ g per immunization.

Use of purified Antigens as subunit vaccines can be carried out by standard methods. For example, the purified protein(s) should be adjusted to an appropriate concentration, formulated with any suitable vaccine adjuvant
35 and packaged for use. Suitable adjuvants may include, but are not limited to: mineral gels, e.g., aluminum hydroxide; surface active substances such as lysolecithin, pluronic

polyols; polyanions; peptides; oil emulsions; alum, and MDP. The immunogen may also be incorporated into liposomes, or conjugated to polysaccharides and/or other polymers for use in a vaccine formulation. In instances where the recombinant
5 Antigen is a hapten, i.e., a molecule that is antigenic in that it can react selectively with cognate antibodies, but not immunogenic in that it cannot elicit an immune response, the hapten may be covalently bound to a carrier or immunogenic molecule; for instance, a large protein such as
10 serum albumin will confer immunogenicity to the hapten coupled to it. The hapten-carrier may be formulated for use as a vaccine.

Effective doses (immunizing amounts) of the vaccines of the invention may also be extrapolated from dose-
15 response curves derived from animal model test systems.

The invention also provides a pharmaceutical pack or kit comprising one or more containers comprising one or more of the ingredients of the vaccine formulations of the invention. Associated with such container(s) can be a notice
20 in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration.

The present invention thus provides a method of
25 immunizing an animal, or treating or preventing various diseases or disorders in an animal, comprising administering to the animal an effective immunizing dose of a vaccine of the present invention.

30 5.11. USE OF ANTIBODIES GENERATED
BY THE VACCINES OF THE INVENTION

The antibodies generated against the Antigen by immunization with the recombinant viruses of the present invention also have potential uses in diagnostic
35 immunoassays, passive immunotherapy, and generation of antiidiotypic antibodies.

The generated antibodies may be isolated by standard techniques known in the art (e.g., immunoaffinity chromatography, centrifugation, precipitation, etc.) and used in diagnostic immunoassays. The antibodies may also be used
5 to monitor treatment and/or disease progression. Any immunoassay system known in the art, such as those listed *supra*, may be used for this purpose including but not limited to competitive and noncompetitive assay systems using techniques such as radioimmunoassays, ELISA (enzyme-linked
10 immunosorbent assays), "sandwich" immunoassays, precipitin reactions, gel diffusion precipitin reactions, immunodiffusion assays, agglutination assays, complement-fixation assays, immunoradiometric assays, fluorescent immunoassays, protein A immunoassays and
15 immunoelectrophoresis assays, to name but a few.

The vaccine formulations of the present invention can also be used to produce antibodies for use in passive immunotherapy, in which short-term protection of a host is achieved by the administration of pre-formed antibody
20 directed against a heterologous organism.

The antibodies generated by the vaccine formulations of the present invention can also be used in the production of antiidiotypic antibody. The antiidiotypic antibody can then in turn be used for immunization, in order
25 to produce a subpopulation of antibodies that bind the initial antigen of the pathogenic microorganism (Jerne, 1974, Ann. Immunol. (Paris) 125c:373; Jerne, et al., 1982, EMBO J. 1:234).

30 6. RECOMBINANT VESICULAR STOMATITIS VIRUSES FROM DNA

We assembled a DNA clone containing the 11,161 nucleotide sequence of the prototype rhabdovirus, vesicular stomatitis virus (VSV), such that it could be transcribed by
35 the bacteriophage T7 RNA polymerase to yield a full-length positive strand RNA complementary to the VSV genome. Expression of this RNA in cells also expressing the VSV

nucleocapsid protein and the two VSV polymerase subunits resulted in production of VSV with the growth characteristics of wild-type VSV. Recovery of virus from DNA was verified by: 1) the presence of two genetic tags
5 generating novel restriction sites in DNA derived from the genome; 2) direct sequencing of the genomic RNA of the recovered virus, and 3), production of a VSV recombinant in which the glycoprotein was derived from a second serotype. The ability to generate VSV from DNA opens numerous
10 possibilities for the genetic analysis of VSV replication. In addition, because VSV can be grown to very high titers and in large quantities with relative ease, one can genetically engineer recombinant VSVs displaying novel antigens. Such modified viruses can be used as vaccines conferring
15 protection against other viruses or pathogenic microorganisms, or to produce immunity in general against an encoded foreign antigen.

6.1. MATERIALS AND METHODS

20 **Plasmid Construction.** The plasmid pVSVFL(+) expressing the 11,161 nucleotide positive strand (antigenomic) VSV RNA sequence was constructed from four DNA fragments cloned into pBluescript SK⁺ (Stratagene). The starting plasmid for the construction, pVSVFL(-), expressed
25 the complete negative sense VSV genomic RNA (Indiana serotype) from a T7 promoter. This plasmid was generated in a nine step cloning procedure that involved joining the five original cDNA clones of the VSV mRNAs (Gallione et al., 1981, J. Virol. 39:529-535; Rose and Gallione, 1981, J. Virol.
30 39:519-528; Schubert et al., 1985, Proc. Natl. Acad. Sci. USA 82:7984-7988) with gene junction fragments and terminal fragments. These fragments were generated by reverse transcription and polymerase chain reaction (RT-PCR) (Mullis and Faloona, 1987, Methods in Enzymology 155:335-350) from
35 VSV genomic RNA (M.A. Whitt, R. Burdine, E.A. Stillman and J.K. Rose, manuscript in preparation). To facilitate engineering of the VSV genome and to provide genetic tags,

unique Mlu I and Nhe I restriction enzyme sites were introduced by oligonucleotide-directed mutagenesis into the 5' and 3' non-coding regions flanking the VSV glycoprotein gene prior to construction of the full length genome.

- 5 In the initial step of constructing pVSVFL(+) we used the primers
 (5'CCGGCTCGAGTTGTAATACGACTCACTATAGGGACGAAGACAAACAAACCATTATTAT
 C-3') (SEQ ID NO:38) and (5'GAACTCTCCTCTAGATGAGAAC-3') (SEQ
 ID NO:39) to amplify (Mullis and Faloona, 1987, Methods in
 10 Enzymology 155:335-350) a 2,124 nucleotide fragment from
 pVSVFL(-) (# 1, Fig. 4A). This fragment corresponds to the
 3' end of the VSV genome. The first primer introduced an Xho
 I site and a T7 promoter (underlined) immediately preceding
 the sequence complementary to the 3' end of the VSV genome.
 15 The second primer covered a unique Xba I site present in the
 VSV P gene. The PCR product was digested with Xho I and Xba
 I and cloned into pBluescript SK⁺ (Stratagene) that had been
 digested with Xho I and Xba I. The resulting plasmid
 carrying the sequence corresponding to the 3' end of the VSV
 20 genome preceded by a T7 promoter was designated pBSXX. Note
 that an additional T7 promoter is also present upstream of
 the Xho I site in the vector. Next we generated the sequence
 corresponding to the 5' end of the VSV genome and part of the
 hepatitis delta virus (HDV) ribozyme (Pattnaik et al., 1992,
 25 Cell 69:1011-1120; Perrotta and Been, 1991, Nature
 350:434-436). A 147 nucleotide PCR product (#3, Fig. 4A) was
 amplified from pVSVFL(-) with primers
 (5'AGGTCGGACCGCGAGGAGGTGGAGATGCCATGCCGACCCACGAAGACCACAAAACCAG
 -3') (SEQ ID NO:40) and (5'ATGTTGAAGAGTGACCTACACG-3') (SEQ ID
 30 NO:41). The first primer contained 39 nucleotides of the
 sequence encoding the HDV ribozyme (underlined) followed by
 19 nucleotides complementary to the 3' end of the VSV
 antigenomic RNA. The second primer hybridized within the L
 gene (Fig. 4A). The PCR product was digested with Afl II and
 35 Rsr II and the 80 nucleotide Afl II-Rsr II fragment was
 ligated to a 225 nucleotide Rsr II-Sac I fragment (#4, Fig.
 4A) derived from a plasmid designated pBS-GMG (Stillman et

al., manuscript submitted). Fragment 4 contained the T7 terminator sequence and the remainder of the sequence encoding the HDV ribozyme. Ligated products were digested with Afl II and Sac I and the 305 nucleotide Afl II-Sac I product was cloned into the Afl II and Sac I sites of a modified pBSXX vector that contained an Afl II site inserted at the unique Not I site within the polylinker. This plasmid containing the Afl II-Sac I fragment was designated pBXXAS. To complete the construction, a 10,077 nucleotide Bst 1107 I to Afl II fragment (#2, Fig. 4A) containing 90% of the VSV sequences from pVSVFL(-) was inserted into the unique Bst 1107 I and AflII sites of pBXXAS. The final plasmid was designated pVSVFL(+). The sequences in this plasmid generated by PCR (hatched sequences, Fig. 4B) were determined and contained no errors. We also prepared a plasmid in which the sequence of the VSV Indiana serotype G gene (MluI-NheI) was replaced with the G gene from the New Jersey serotype of VSV (Gallione and Rose, 1983, J. Virol. 46:162-169). This plasmid is called pVSVFL(+)_{INJG} and has only a single T7 promoter.

Transfection and recovery of recombinant VSV. Baby hamster kidney cells (BHK-21, ATCC) were maintained in DME (Dulbecco's modified Eagle's medium) supplemented with 5% fetal bovine serum (FBS). Cells on 10 cm dishes (~70% confluent) were infected at a multiplicity of 10 with vTF7-3 (Fuerst et al., 1986, Proc. Natl. Acad. Sci. USA 83:8122-8126). After 30 min, plasmids encoding the VSV antigenomic RNA and the N, P, and L proteins were transfected into the cells using a calcium phosphate transfection kit according to directions supplied (Stratagene). The coding regions for N, P, and L proteins were each expressed in pBluescript SK(+) from the T7 promoter. Plasmid amounts were 10 µg pVSVFL(+), 5 µg pBS-N, 4 µg pBS-P, and 2 µg pBS-L. After 24-48 h incubation at 37°C in 3% CO₂, cells were scraped from the dish and subjected to three rounds of freeze-thawing (-70°C, 37°C) to release cell-associated virus. Debris was pelleted from the cell lysates by

centrifugation at 1,250 x g for 5 min. Five ml of this lysate was added to approximately 10^6 BHK cells on a 10 cm plate in 10 ml of DME + 5% FBS. After 48 h the medium was clarified by centrifugation at 1,250 x g for 10 min, and
5 passed through a filter to remove the majority of the vaccinia virus (0.2 μ m pore size, Gelman Sciences). One ml was then added directly to BHK cells that had been plated on a coverslip in a 35 mm dish. After four hours, the cells were fixed in 3% paraformaldehyde and stained with monoclonal
10 antibody I1 to the VSV G₁ protein (Lefrancois and Lyles, 1982, Virology 121:168-174) or 9B5 (Bricker et al., 1987, Virology 161:533-540) to the VSV G_N protein followed by goat anti-mouse rhodamine conjugated antibody (Jackson Research). Cells were then examined by indirect immunofluorescence using a Nikon
15 Microphot-FX microscope equipped with a 40x planapochromat objective. When VSV recovery was successful, 100% of the cells showed the typical bright stain for G protein characteristic of a VSV infection.

Preparation and analysis of VSV RNA and protein.

20 Recombinant VSV and wild-type VSV isolated from single plaques ($\sim 10^5$ plaque forming units) were used to infect a monolayer of BHK cells ($\sim 80\%$ confluent) on a 10 cm dish in 10 ml DME plus 5% FBS. After 24 h, cell debris and nuclei were removed by centrifugation at 1,250 x g for 5 min, and
25 virus was then pelleted from the medium at 35,000 RPM in a Beckman SW41 rotor for one hour. Virus pellets were resuspended in 0.5 ml 10 mM Tris-HCl, pH 7.4 for protein analysis. For RNA isolation, virus was resuspended in 0.2 ml of 0.5% SDS/0.2M sodium acetate, pH 8.0, followed by
30 extraction with phenol/ CHCl_3 . RNA was precipitated with 95% ethanol and 5 μ g carrier tRNA. RNA was pelleted by centrifugation at 12,000 x g for 15 min and resuspended in water with 1 unit RNasin (Promega). For analysis of RNA by
35 RT-PCR, primer pairs flanking either the novel Nhe I or Mlu I sites were used. The first strand DNA synthesis reaction was carried out in 50 μ l of PCR buffer (Promega) containing 5 mM MgCl_2 , 1 mM dNTPs, 1 unit RNAs in (Promega), 1 unit avian

myeloblastosis virus reverse transcriptase (AMV RT; Promega) 0.75 μ M primer and approximately 0.25 μ g of VSV genomic RNA. Incubation was at 42°C for 15 min followed by 5 min at 99°C and 5 min at 5°C. PCR was carried out by addition of 0.5 U 5 Tag polymerase, adjustment of MgCl₂ concentration to 1.25 mM, and addition of the second primer (0.75 μ M). The reaction was subjected to 20 thermal cycles: 95°C, 1 min; 60°C 1.5 min. The reaction was then incubated at 60°C for 7 min.

Direct sequencing of VSV genomic RNA was performed according to a previously described protocol based on the dideoxy chain termination method (Mierendorf and Pfeffer, 1987, Methods in Enzymology 152:563-566) except that [α -³³P]dATP (Amersham, Inc.) was used. Each reaction included approximately 0.25 μ g of VSV genomic RNA.

15

6.2. RESULTS

To construct a cDNA clone encoding the entire 11,161 VSV genome, individual cDNA clones of the VSV mRNAs were initially joined using small DNA fragments generated by 20 RT-PCR that covered the four gene junctions. Correct genomic terminal sequences were also generated by RT-PCR of the VSV genome, and these were joined to the other DNAs using restriction sites. This initial clone was constructed with a T7 promoter directing synthesis of the full-length negative 25 strand VSV RNA. Despite numerous attempts, we were unable to recover VSV from cells expressing the VSV genomic RNA and the VSV N, P, and L proteins. The VSV constructed was thus redesigned to express the VSV antigenomic DNA. The construction strategy is described in Materials and Methods 30 and in Fig. 4A-B. The entire VSV sequence as well as a T7 promoter, terminator and HDV ribozyme sequence were cloned in pBluescript SK+ between the Xho I and Sac I sites (Fig. 4B; Fig. 1). An additional T7 promoter is also present upstream of the Xho I site in the plasmid. A slightly different 35 cloning strategy was used to generate plasmids lacking the upstream T7 promoter and VSV has also been recovered from these constructs.

Recovery of VSV from DNA. To determine if we could recover VSV from plasmid DNA, we infected cells with vaccinia vTF7-3 (Fuerst et al., 1986, Proc. Natl. Acad. Sci. USA 83:8122-8126) to provide cytoplasmic T7 RNA polymerase.

- 5 These cells were then transfected with pVSVFL(+), which expresses the antigenomic VSV RNA from a T7 promoter, and three other plasmids which express the VSV N, P, and L proteins. Expression of the N protein was required to assemble nascent VSV antigenomic RNA into nucleocapsids.
- 10 Once formed, these nucleocapsids should serve as templates for synthesis of minus strand RNA by the L/P polymerase complex. Encapsidated minus strand RNA should then be a template for transcription, initiating the VSV infectious cycle.
- 15 The initial recovery experiment employed two 10 cm plates of BHK cells ($\sim 5 \times 10^6$ cells each). At 24 hours after the infection with vTF7-3 and transfection with the four plasmids, cells and medium were frozen and thawed to release any cell-associated VSV, and the clarified lysates were added
- 20 to fresh BHK cells. After 48 hours, both plates showed severe cytopathic effects that could have been due either to vaccinia virus or to recovered VSV. One ml of each supernatant was then added to small dishes of BHK cells on coverslips. After two hours, one of these coverslips showed
- 25 rounded cells characteristic of a VSV infection, while the other did not. After 4 hours, cells on both coverslips were fixed, stained with appropriate antibodies, and examined by indirect immunofluorescence microscopy to detect the VSV G protein. All cells on the coverslip showing rounded cells
- 30 revealed intense fluorescence characteristic of G protein expression during VSV infection (data not shown). Subsequent passaging and analysis described below showed that VSV had been recovered from the transfection. The other coverslip showed no G expression, and no VSV could be recovered after
- 35 passaging.

Based on the frequency with which rabies virus (Schnell et al., 1994, EMBO J. 13:4195-4203) and VSV

minigenomes (Stillman et al., manuscript submitted) were recovered, we anticipated that recovery of complete VSV, if obtainable, would be a rare event. The initial recovery of VSV from only one of two transfections suggested the possibility that the initial titer in the positive lysate was very low. To examine this titer, we infected BHK cells on coverslips with one tenth of the lysate (1 ml) derived from each initial transfection. After eight hours, the cells were examined for expression of G protein by indirect immunofluorescence. A scan of the entire coverslip revealed no VSV infection from the negative lysate, and only five small areas of infection (2-6 cells each) from the lysate that gave rise to VSV G expression on subsequent passaging. The initial titer was therefore very low as we suspected, and likely represented a total of about 50 infectious particles, probably derived from a VSV infection initiated in only one cell out of 2×10^7 transfected. This low rate of recovery of infectious VSV is typical of that observed in several experiments.

Analysis of viral proteins. Subsequent passages and plaque assays of VSV recovered in three independent experiments revealed plaques that were detectable in less than 16 hours and titers up to 2×10^9 pfu/ml characteristic of VSV. For further verification that VSV had been recovered, the proteins in virus pelleted from the medium were examined by SDS polyacrylamide gel electrophoresis (PAGE). Fig. 5 shows the Coomassie stained gel of proteins of VSV recovered from recombinant DNA (rVSV) and wildtype VSV. The mobilities and relative amounts of the five viral proteins were indistinguishable in the wildtype and recombinant virus.

Identification of sequence tags. In pVSVFL(+), the VSV nucleotide sequence was altered by oligonucleotide-directed mutagenesis to generate unique Mlu I and Nhe I restriction enzyme sites in the 5' and 3' non-coding regions of the glycoprotein gene. To verify that these sites were present in recovered virus, we carried out reverse

transcription of genomic RNA purified from wild-type or recombinant virions using primers upstream of each restriction site. The reverse transcription products were then amplified by PCR using an additional primer downstream of each restriction site. The presence of the genetic tag in the recombinant virus was verified by digestion of the PCR products with the appropriate restriction enzymes. Using this method, the presence of both the Mlu I and Nhe I sequences in the recovered virus RNA was verified, and the results for the Nhe I site are shown in Fig. 6. Sequences from wild-type VSV and recombinant VSV were amplified in parallel and a 620 nucleotide fragment was obtained in both cases (lanes 3 and 5). No product was obtained when reverse transcriptase was omitted from the reactions prior to PCR (lanes 1 and 2), indicating that the PCR product was derived from RNA, not from contaminating DNA. After digestion with Nhe I, expected fragments of 273 and 347 base pairs were obtained from recombinant VSV RNA, while the DNA derived from the wildtype RNA remained undigested (lanes 4 and 6).

Direct sequencing of tagged genomic RNA. The presence of new restriction sites in the DNA generated by PCR provided strong evidence that VSV had been recovered from DNA. To ensure that identification of the genetic tags by PCR had not resulted from inadvertent contamination by plasmid DNA, we carried out direct sequence analysis of the genomic RNA using reverse transcriptase and a primer hybridizing upstream of the Nhe I site. The sequence from the autoradiogram shown in Fig. 7 is in exact agreement with the published sequence of the VSV G mRNA (Rose and Gallione, 1981, J. Virol. 39:519-528) except that the four nucleotide changes used to generate the Nhe I site (GCACAA to GCTAGC) are present. These results show unequivocally that the sequence tag is present in the genomic RNA.

Recombinant VSV Indiana virus carrying the glycoprotein of the New Jersey serotype. There are two serotypes of VSV designated Indiana and New Jersey. The glycoproteins of the two serotypes share approximately 50%

sequence identity (Gallione and Rose, 1983, J. Virol. 46:162-169). In earlier studies we found that the glycoprotein of the New Jersey serotype could complement a mutant of the VSV_I serotype that makes a defective glycoprotein (Whitt et al., 1989, J. Virol. 63:3569-3578). It therefore seemed likely that a recombinant VSV in which the Indiana glycoprotein (G_I) gene was replaced by the New Jersey glycoprotein (G_{NJ}) gene would be viable despite the extensive sequence divergence. To generate such a recombinant, the G_{NJ} cDNA was amplified by PCR using primers that introduced Mlu I and Nhe I sites within the 5' and 3' non-coding regions at each end of the gene. The amplified DNA was cloned into pBluescript and the G_{NJ} protein was expressed in BHK cells using the vaccinia-T7 system. The protein expressed was shown to have membrane fusion activity below pH 6.0 indicating that it was functional (data not shown). This G_{NJ} cDNA was then cloned into the unique Mlu I and Nhe I sites of the full-length construct after removal of sequences encoding G_I. Recombinant VSV was recovered essentially as described above except that the initial transfection was allowed to proceed for 48 hours before the freeze-thaw step. After the first passage, expression of the G_{NJ} protein was verified by indirect immunofluorescence using a monoclonal antibody specific to G_{NJ} (Bricker et al., 1987, Virology 161:533-540). The virus was then plaque purified and grown. To examine the proteins present in the recombinant virus, virus recovered from cells infected with VSV_I, VSV_{NJ}, and the recombinant VSV_{I/NJG} was analyzed by SDS-PAGE followed by Coomassie staining. The VSV_I G, N, P, and M proteins each have mobilities distinct from their VSV_{NJ} counterparts (Fig. 8, lanes 1 and 3). The recombinant VSV_{I/NJG} shows the mobility difference in only the G protein as expected (lane 2). The presence of the novel Nhe I and Mlu I sites in the recombinant was also verified (data not shown).

35

6.3. DISCUSSION

The results presented here establish that infectious VSV can be recovered from recombinant DNA. We believe that expressing the positive strand, antigenomic RNA 5 in the presence of the N, P and L proteins was critical to our success because we have not recovered virus starting with an equivalent construct encoding the genomic RNA.

Why is the initial event of generating VSV so rare, apparently occurring in only 1 in 10^7 to 10^8 transfected cells? 10 One possibility is that our clone contains a sequence error that is only corrected by a rare mutational event. We believe this is not the case because the clone was completely sequenced prior to assembly and differences from published sequences were corrected, or the proteins were shown to be 15 functional in complementation assays. Also, the frequency of recovery is actually higher than expected based on our observations with minigenomes encoding one or two VSV proteins (Stillman et al., manuscript submitted). In these cases we found that a transcribing and replicating minigenome 20 (~2kb RNA) was recovered in about 1 in 10^2 transfected cells expressing the RNA with the N, P and L proteins. Addition of a second cistron (0.85 kb additional RNA) encoding the M protein dropped the recovery rate to approximately 1 in 10^3 transfected cells. If there is a ten-fold drop in recovery 25 rate for each additional kilobase of RNA added, one can easily rationalize an even lower frequency of recovery for the 11, 161 kb genome than we observed. Although these minigenomes encode negative sense RNAs, the comparison of the frequency of recovery to that of the full length plus 30 construct is probably valid because expression of the N, P and L mRNAs would not generate mRNAs complementary to the minigenome.

Although the rate limiting step in generation of infectious VSV is not known, it is likely to be at the level 35 of synthesis and encapsidation of the large antigenomic RNA, which must occur prior to replication and transcription. The complete encapsidation with N protein probably has to occur

on the nascent RNA to protect it from degradation, and the cells in which this occurs must also produce appropriate amounts of L and P proteins to initiate replication. Once this has occurred, however, the transcription and translation of the genome should generate additional N, P, and L proteins as well as the G and M proteins required for budding of infectious virus.

The recovery of VSV from DNA opens numerous aspects of the viral life cycle to genetic analysis. The studies of the genetic signals involved in transcription and replication have so far been confined to analysis of defective RNAs that do not encode viral proteins (Pattnaik et al., 1992, Cell 69:1011-1120; Wertz et al., 1994, Proc. Natl. Acad. Sci. USA 91:8587-8591). These and other signals can be now examined in the context of a VSV infection occurring in the absence of a vaccinia virus infection. The system we have described also provides an opportunity to study the roles of individual viral protein domains and modifications in viral assembly and replication. Previously these analyses have been confined to in vitro systems or to analysis employing the complementation of naturally occurring mutants where synthesis of the mutant protein can complicate the analysis.

Perhaps even more exciting is the ability to use VSV as a vector to express other proteins. The experiment in which we recovered VSV Indiana carrying the glycoprotein from the New Jersey serotype (Fig. 8) illustrates that viable recombinants can be made. For reasons that are unclear the titers of recombinant virus were at least ten-fold lower than those obtained with either parent. The lower titer apparently did not result from a defect in viral assembly because the amounts of proteins in wildtype and recombinant virions at the end of the infection were comparable (Fig. 8). Our previous experiments showed that a foreign glycoprotein carrying the appropriate cytoplasmic tail signal could be incorporated into the VSV envelope (Owens and Rose, 1993, J. Virol. 67:360-365). This suggests that one may generate recombinant VSVs carrying novel proteins in their envelopes.

If these were appropriately attenuated, they can be used as vaccines against other viral diseases.

The truncated genomes of defective interfering particles are replicated and packaged very well, thus we
5 suspect that there will be flexibility in the maximum length of the genome that can be packaged as well. Presumably a longer nucleocapsid can be packaged as a longer bullet-shaped particle. Because of the modular nature of the VSV genome, with conserved gene end and start sequences at the gene
10 junctions (Rose and Schubert, 1987, in *The Viruses: The Rhabdoviruses*, Plenum Publishing Corp., NY, pp. 129-166), it should be relatively easy to engineer additional genes into VSV.

15

7. DEPOSIT OF MICROORGANISMS

Plasmid pVSVFL(+) was deposited on May 2, 1995 with the American Type Culture Collection (ATCC), 1201 Parklawn Drive, Rockville, Maryland 20852, under the provisions of the Budapest Treaty on the International Recognition of the
20 Deposit of Microorganisms for the Purposes of Patent Procedures, and assigned accession no. 97134.

The present invention is not to be limited in scope by the microorganism deposited or the specific embodiments
25 described herein. Indeed, various modifications of the invention in addition to those described herein will become apparent to those skilled in the art from the foregoing description and accompanying figures. Such modifications are intended to fall within the scope of the appended claims.

30

Various publications are cited herein, the disclosures of which are incorporated by reference in their entireties.

35

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Rose, John K.
- (ii) TITLE OF INVENTION: RECOMBINANT VESICULOVIRUSES AND THEIR USES
- (iii) NUMBER OF SEQUENCES: 41
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: PENNIE & EDMONDS
 - (B) STREET: 1155 Avenue of the Americas
 - (C) CITY: New York
 - (D) STATE: New York
 - (E) COUNTRY: USA
 - (F) ZIP: 10036-2711
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: To Be Assigned
 - (B) FILING DATE: On Even Date Herewith
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Misrock, S. Leslie
 - (B) REGISTRATION NUMBER: 18,872
 - (C) REFERENCE/DOCKET NUMBER: 6523-009-228
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 - (C) TELEX: 66141 PENNIE

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14311 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 760..2025
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2092..2886
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2946..3632
- (ix) FEATURE:
 - (A) NAME/KEY: CDS

(B) LOCATION: 3774..5306

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 5429..11755

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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CTCATTTTTT AACCAATAGG CCGAAATCGG CAAAATCCCT TATAAATCAA AAGAATAGAC	120
CGAGATAGGG TTGAGTGTG TTCCAGTTT GAACAAGAGT CCACTATTAA AGAACGTGGA	180
CTCCAACGTC AAAGGGCGAA AAACCGTCTA TCAGGGCGAT GGCCCACTAC GTGAACCATC	240
ACCCTAATCA AGTTTTTTGG GGTGAGGTG CCGTAAAGCA CTAAATCGGA ACCCTAAAGG	300
GAGCCCCCGA TTTAGAGCTT GACGGGGAAA GCCGGCGAAC GTGGCGAGAA AGGAAGGGAA	360
GAAAGCGAAA GGAGCGGGCG CTAGGGCGCT GGCAAGTGTA GCGGTCACGC TCGCGTAAC	420
CACCACACCC GCCGCGCTTA ATGCGCCGCT ACAGGGCGCG TCCCATTCGC CATTGAGGCT	480
GCGCAACTGT TGGGAAGGGC GATCGGTGCG GGCCTCTTCG CTATTACGCC AGCTGGCGAA	540
AGGGGGATGT GCTGCAAGGC GATTAAGTTG GGTAACGCCA GGGTTTTCCC AGTCACGACG	600
TTGTAAAACG ACGGCCAGTG AATTGTAATA CGACTCACTA TAGGGCGAAT TGGGTACCGG	660
GCCCCCCTC GAGTTGTAAT ACGACTCACT ATAGGGACGA AGACAAACAA ACCATTATTA	720
TCATTAAAAG GCTCAGGAGA AACTTTAACA GTAATCAAA ATG TCT	774
Met Ser Val Thr Val	
1 5	
AAG AGA ATC ATT GAC AAC ACA GTC ATA GTT CCA AAA CTT CCT GCA AAT	822
Lys Arg Ile Ile Asp Asn Thr Val Ile Val Pro Lys Leu Pro Ala Asn	
10 15 20	
GAG GAT CCA GTG GAA TAC CCG GCA GAT TAC TTC AGA AAA TCA AAG GAG	870
Glu Asp Pro Val Glu Tyr Pro Ala Asp Tyr Phe Arg Lys Ser Lys Glu	
25 30 35	
ATT CCT CTT TAC ATC AAT ACT ACA AAA AGT TTG TCA GAT CTA AGA GGA	918
Ile Pro Leu Tyr Ile Asn Thr Thr Lys Ser Leu Ser Asp Leu Arg Gly	
40 45 50	
TAT GTC TAC CAA GGC CTC AAA TCC GGA AAT GTA TCA ATC ATA CAT GTC	966
Tyr Val Tyr Gln Gly Leu Lys Ser Gly Asn Val Ser Ile Ile His Val	
55 60 65	
AAC AGC TAC TTG TAT GGA GCA TTA AAG GAC ATC CGG GGT AAG TTG GAT	1014
Asn Ser Tyr Leu Tyr Gly Ala Leu Lys Asp Ile Arg Gly Lys Leu Asp	
70 75 80 85	
AAA GAT TGG TCA AGT TTC GGA ATA AAC ATC GGG AAA GCA GGG GAT ACA	1062
Lys Asp Trp Ser Ser Phe Gly Ile Asn Ile Gly Lys Ala Gly Asp Thr	
90 95 100	
ATC GGA ATA TTT GAC CTT GTA TCC TTG AAA GCC CTG GAC GGC GTA CTT	1110
Ile Gly Ile Phe Asp Leu Val Ser Leu Lys Ala Leu Asp Gly Val Leu	
105 110 115	
CCA GAT GGA GTA TCG GAT GCT TCC AGA ACC AGC GCA GAT GAC AAA TGG	1158
Pro Asp Gly Val Ser Asp Ala Ser Arg Thr Ser Ala Asp Asp Lys Trp	

120	125	130	
TTG CCT TTG TAT CTA CTT GGC TTA TAC AGA GTG GGC AGA ACA CAA ATG Leu Pro Leu Tyr Leu Leu Gly Leu Tyr Arg Val Gly Arg Thr Gln Met 135 140 145			1206
CCT GAA TAC AGA AAA AAG CTC ATG GAT GGG CTG ACA AAT CAA TGC AAA Pro Glu Tyr Arg Lys Lys Leu Met Asp Gly Leu Thr Asn Gln Cys Lys 150 155 160 165			1254
ATG ATC AAT GAA CAG TTT GAA CCT CTT GTG CCA GAA GGT CGT GAC ATT Met Ile Asn Glu Gln Phe Glu Pro Leu Val Pro Glu Gly Arg Asp Ile 170 175 180			1302
TTT GAT GTG TGG GGA AAT GAC AGT AAT TAC ACA AAA ATT GTC GCT GCA Phe Asp Val Trp Gly Asn Asp Ser Asn Tyr Thr Lys Ile Val Ala Ala 185 190 195			1350
GTG GAC ATG TTC TTC CAC ATG TTC AAA AAA CAT GAA TGT GCC TCG TTC Val Asp Met Phe Phe His Met Phe Lys Lys His Glu Cys Ala Ser Phe 200 205 210			1398
AGA TAC GGA ACT ATT GTT TCC AGA TTC AAA GAT TGT GCT GCA TTG GCA Arg Tyr Gly Thr Ile Val Ser Arg Phe Lys Asp Cys Ala Ala Leu Ala 215 220 225			1446
ACA TTT GGA CAC CTC TGC AAA ATA ACC GGA ATG TCT ACA GAA GAT GTA Thr Phe Gly His Leu Cys Lys Ile Thr Gly Met Ser Thr Glu Asp Val 230 235 240 245			1494
ACG ACC TGG ATC TTG AAC CGA GAA GTT GCA GAT GAA ATG GTC CAA ATG Thr Thr Trp Ile Leu Asn Arg Glu Val Ala Asp Glu Met Val Gln Met 250 255 260			1542
ATG CTT CCA GGC CAA GAA ATT GAC AAG GCC GAT TCA TAC ATG CCT TAT Met Leu Pro Gly Gln Glu Ile Asp Lys Ala Asp Ser Tyr Met Pro Tyr 265 270 275			1590
TTG ATC GAC TTT GGA TTG TCT TCT AAG TCT CCA TAT TCT TCC GTC AAA Leu Ile Asp Phe Gly Leu Ser Ser Lys Ser Pro Tyr Ser Ser Val Lys 280 285 290			1638
AAC CCT GCC TTC CAC TTC TGG GGG CAA TTG ACA GCT CTT CTG CTC AGA Asn Pro Ala Phe His Phe Trp Gly Gln Leu Thr Ala Leu Leu Leu Arg 295 300 305			1686
TCC ACC AGA GCA AGG AAT GCC CGA CAG CCT GAT GAC ATT GAG TAT ACA Ser Thr Arg Ala Arg Asn Ala Arg Gln Pro Asp Asp Ile Glu Tyr Thr 310 315 320 325			1734
TCT CTT ACT ACA GCA GGT TTG TTG TAC GCT TAT GCA GTA GGA TCC TCT Ser Leu Thr Thr Ala Gly Leu Leu Tyr Ala Tyr Ala Val Gly Ser Ser 330 335 340			1782
GCC GAC TTG GCA CAA CAG TTT TGT GTT GGA GAT AAC AAA TAC ACT CCA Ala Asp Leu Ala Gln Gln Phe Cys Val Gly Asp Asn Lys Tyr Thr Pro 345 350 355			1830
GAT GAT AGT ACC GGA GGA TTG ACG ACT AAT GCA CCG CCA CAA GGC AGA Asp Asp Ser Thr Gly Gly Leu Thr Thr Asn Ala Pro Pro Gln Gly Arg 360 365 370			1878
GAT GTG GTC GAA TGG CTC GGA TGG TTT GAA GAT CAA AAC AGA AAA CCG Asp Val Val Glu Trp Leu Gly Trp Phe Glu Asp Gln Asn Arg Lys Pro 375 380 385			1926
ACT CCT GAT ATG ATG CAG TAT GCG AAA AGA GCA GTC ATG TCA CTG CAA			1974

Thr Pro Asp Met Met Gln Tyr Ala Lys Arg Ala Val Met Ser Leu Gln 390 395 400 405	
GGC CTA AGA GAG AAG ACA ATT GGC AAG TAT GCT AAG TCA GAA TTT GAC Gly Leu Arg Glu Lys Thr Ile Gly Lys Tyr Ala Lys Ser Glu Phe Asp 410 415 420	2022
AAA TGA CCCTATAATT CTCAGATCAC CTATTATATA TTATGCTACA TATGAAAAA Lys	2078
ACTAACAGAT ATC ATG GAT AAT CTC ACA AAA GTT CGT GAG TAT CTC AAG Met Asp Asn Leu Thr Lys Val Arg Glu Tyr Leu Lys 1 5 10	2127
TCC TAT TCT CGT CTG GAT CAG GCG GTA GGA GAG ATA GAT GAG ATC GAA Ser Tyr Ser Arg Leu Asp Gln Ala Val Gly Glu Ile Asp Glu Ile Glu 15 20 25	2175
GCA CAA CGA GCT GAA AAG TCC AAT TAT GAG TTG TTC CAA GAG GAT GGA Ala Gln Arg Ala Glu Lys Ser Asn Tyr Glu Leu Phe Gln Glu Asp Gly 30 35 40	2223
GTG GAA GAG CAT ACT AAG CCC TCT TAT TTT CAG GCA GCA GAT GAT TCT Val Glu Glu His Thr Lys Pro Ser Tyr Phe Gln Ala Ala Asp Asp Ser 45 50 55 60	2271
GAC ACA GAA TCT GAA CCA GAA ATT GAA GAC AAT CAA GGT TTG TAT GCA Asp Thr Glu Ser Glu Pro Glu Ile Glu Asp Asn Gln Gly Leu Tyr Ala 65 70 75	2319
CCA GAT CCA GAA GCT GAG CAA GTT GAA GGC TTT ATA CAG GGG CCT TTA Pro Asp Pro Glu Ala Glu Gln Val Glu Gly Phe Ile Gln Gly Pro Leu 80 85 90	2367
GAT GAC TAT GCA GAT GAG GAA GTG GAT GTT GTA TTT ACT TCG GAC TGG Asp Asp Tyr Ala Asp Glu Glu Val Asp Val Val Phe Thr Ser Asp Trp 95 100 105	2415
AAA CAG CCT GAG CTT GAA TCT GAC GAG CAT GGA AAG ACC TTA CGG TTG Lys Gln Pro Glu Leu Glu Ser Asp Glu His Gly Lys Thr Leu Arg Leu 110 115 120	2463
ACA TCG CCA GAG GGT TTA AGT GGA GAG CAG AAA TCC CAG TGG CTT TCG Thr Ser Pro Glu Gly Leu Ser Gly Glu Gln Lys Ser Gln Trp Leu Ser 125 130 135 140	2511
ACG ATT AAA GCA GTC GTG CAA AGT GCC AAA TAC TGG AAT CTG GCA GAG Thr Ile Lys Ala Val Val Gln Ser Ala Lys Tyr Trp Asn Leu Ala Glu 145 150 155	2559
TGC ACA TTT GAA GCA TCG GGA GAA GGG GTC ATT ATG AAG GAG CGC CAG Cys Thr Phe Glu Ala Ser Gly Glu Gly Val Ile Met Lys Glu Arg Gln 160 165 170	2607
ATA ACT CCG GAT GTA TAT AAG GTC ACT CCA GTG ATG AAC ACA CAT CCG Ile Thr Pro Asp Val Tyr Lys Val Thr Pro Val Met Asn Thr His Pro 175 180 185	2655
TCC CAA TCA GAA GCA GTA TCA GAT GTT TGG TCT CTC TCA AAG ACA TCC Ser Gln Ser Glu Ala Val Ser Asp Val Trp Ser Leu Ser Lys Thr Ser 190 195 200	2703
ATG ACT TTC CAA CCC AAG AAA GCA AGT CTT CAG CCT CTC ACC ATA TCC Met Thr Phe Gln Pro Lys Lys Ala Ser Leu Gln Pro Leu Thr Ile Ser 205 210 215 220	2751

TTG GAT GAA TTG TTC TCA TCT AGA GGA GAG TTC ATC TCT GTC GGA GGT Leu Asp Glu Leu Phe Ser Ser Arg Gly Glu Phe Ile Ser Val Gly Gly 225 230 235	2799
GAC GGA CGA ATG TCT CAT AAA GAG GCC ATC CTG CTC GGC CTG AGA TAC Asp Gly Arg Met Ser His Lys Glu Ala Ile Leu Leu Gly Leu Arg Tyr 240 245 250	2847
AAA AAG TTG TAC AAT CAG GCG AGA GTC AAA TAT TCT CTG TAG Lys Lys Leu Tyr Asn Gln Ala Arg Val Lys Tyr Ser Leu 255 260 265	2889
ACTATGAAAA AAAGTAACAG ATATCACGAT CTAAGTGTGA TCCCAATCCA TTCATC	2945
ATG AGT TCC TTA AAG AAG ATT CTC GGT CTG AAG GGG AAA GGT AAG AAA Met Ser Ser Leu Lys Lys Ile Leu Gly Leu Lys Gly Lys Gly Lys Lys 1 5 10 15	2993
TCT AAG AAA TTA GGG ATC GCA CCA CCC CCT TAT GAA GAG GAC ACT AGC Ser Lys Lys Leu Gly Ile Ala Pro Pro Pro Tyr Glu Glu Asp Thr Ser 20 25 30	3041
ATG GAG TAT GCT CCG AGC GCT CCA ATT GAC AAA TCC TAT TTT GGA GTT Met Glu Tyr Ala Pro Ser Ala Pro Ile Asp Lys Ser Tyr Phe Gly Val 35 40 45	3089
GAC GAG ATG GAC ACC TAT GAT CCG AAT CAA TTA AGA TAT GAG AAA TTC Asp Glu Met Asp Thr Tyr Asp Pro Asn Gln Leu Arg Tyr Glu Lys Phe 50 55 60	3137
TTC TTT ACA GTG AAA ATG ACG GTT AGA TCT AAT CGT CCG TTC AGA ACA Phe Phe Thr Val Lys Met Thr Val Arg Ser Asn Arg Pro Phe Arg Thr 65 70 75 80	3185
TAC TCA GAT GTG GCA GCC GCT GTA TCC CAT TGG GAT CAC ATG TAC ATC Tyr Ser Asp Val Ala Ala Val Ser His Trp Asp His Met Tyr Ile 85 90 95	3233
GGA ATG GCA GGG AAA CGT CCC TTC TAC AAA ATC TTG GCT TTT TTG GGT Gly Met Ala Gly Lys Arg Pro Phe Tyr Lys Ile Leu Ala Phe Leu Gly 100 105 110	3281
TCT TCT AAT CTA AAG GCC ACT CCA GCG GTA TTG GCA GAT CAA GGT CAA Ser Ser Asn Leu Lys Ala Thr Pro Ala Val Leu Ala Asp Gln Gly Gln 115 120 125	3329
CCA GAG TAT CAC ACT CAC TGC GAA GGC AGG GCT TAT TTG CCA CAT AGG Pro Glu Tyr His Thr His Cys Glu Gly Arg Ala Tyr Leu Pro His Arg 130 135 140	3377
ATG GGG AAG ACC CCT CCC ATG CTC AAT GTA CCA GAG CAC TTC AGA AGA Met Gly Lys Thr Pro Pro Met Leu Asn Val Pro Glu His Phe Arg Arg 145 150 155 160	3425
CCA TTC AAT ATA GGT CTT TAC AAG GGA ACG ATT GAG CTC ACA ATG ACC Pro Phe Asn Ile Gly Leu Tyr Lys Gly Thr Ile Glu Leu Thr Met Thr 165 170 175	3473
ATC TAC GAT GAT GAG TCA CTG GAA GCA GCT CCT ATG ATC TGG GAT CAT Ile Tyr Asp Asp Glu Ser Leu Glu Ala Ala Pro Met Ile Trp Asp His 180 185 190	3521
TTC AAT TCT TCC AAA TTT TCT GAT TTC AGA GAG AAG GCC TTA ATG TTT Phe Asn Ser Ser Lys Phe Ser Asp Phe Arg Glu Lys Ala Leu Met Phe 195 200 205	3569
GGC CTG ATT GTC GAG AAA AAG GCA TCT GGA GCG TGG GTC CTG GAT TCT	3617

Gly Leu Ile Val Glu Lys Lys Ala Ser Gly Ala Trp Val Leu Asp Ser
 210 215 220
 ATC AGC CAC TTC AAA TGA GCTAGTCTAA CTTCTAGCTT CTGAACAATC 3665
 Ile Ser His Phe Lys
 225
 CCCGGTTTAC TCAGTCTCTC CTAATTCCAG CCTCTCGAAC AACTAATATC CTGTCTTTTC 3725
 TATCCCTATG AAAAAAATA ACAGAGATCG ATCTGTTTAC GCGTCACT ATG AAG TGC 3782
 Met Lys Cys
 1
 CTT TTG TAC TTA GCC TTT TTA TTC ATT GGG GTG AAT TGC AAG TTC ACC 3830
 Leu Leu Tyr Leu Ala Phe Leu Phe Ile Gly Val Asn Cys Lys Phe Thr
 5 10 15
 ATA GTT TTT CCA CAC AAC CAA AAA GGA AAC TGG AAA AAT GTT CCT TCT 3878
 Ile Val Phe Pro His Asn Gln Lys Gly Asn Trp Lys Asn Val Pro Ser
 20 25 30 35
 AAT TAC CAT TAT TGC CCG TCA AGC TCA GAT TTA AAT TGG CAT AAT GAC 3926
 Asn Tyr His Tyr Cys Pro Ser Ser Ser Asp Leu Asn Trp His Asn Asp
 40 45 50
 TTA ATA GGC ACA GCC ATA CAA GTC AAA ATG CCC AAG AGT CAC AAG GCT 3974
 Leu Ile Gly Thr Ala Ile Gln Val Lys Met Pro Lys Ser His Lys Ala
 55 60 65
 ATT CAA GCA GAC GGT TGG ATG TGT CAT GCT TCC AAA TGG GTC ACT ACT 4022
 Ile Gln Ala Asp Gly Trp Met Cys His Ala Ser Lys Trp Val Thr Thr
 70 75 80
 TGT GAT TTC CGC TGG TAT GGA CCG AAG TAT ATA ACA CAG TCC ATC GGA 4070
 Cys Asp Phe Arg Trp Tyr Gly Pro Lys Tyr Ile Thr Gln Ser Ile Arg
 85 90 95
 TCC TTC ACT CCA TCT GTA GAA CAA TGC AAG GAA AGC ATT GAA CAA ACG 4118
 Ser Phe Thr Pro Ser Val Glu Gln Cys Lys Glu Ser Ile Glu Gln Thr
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 Lys Gln Gly Thr Trp Leu Asn Pro Gly Phe Pro Pro Gln Ser Cys Gly
 120 125 130
 TAT GCA ACT GTG ACG GAT GCC GAA GCA GTG ATT GTC CAG GTG ACT CCT 4214
 Tyr Ala Thr Val Thr Asp Ala Glu Ala Val Ile Val Gln Val Thr Pro
 135 140 145
 CAC CAT GTG CTG GTT GAT GAA TAC ACA GGA GAA TGG GTT GAT TCA CAG 4262
 His His Val Leu Val Asp Glu Tyr Thr Gly Glu Trp Val Asp Ser Gln
 150 155 160
 TTC ATC AAC GGA AAA TGC AGC AAT TAC ATA TGC CCC ACT GTC CAT AAC 4310
 Phe Ile Asn Gly Lys Cys Ser Asn Tyr Ile Cys Pro Thr Val His Asn
 165 170 175
 TCT ACA ACC TGG CAT TCT GAC TAT AAG GTC AAA GGG CTA TGT GAT TCT 4358
 Ser Thr Thr Trp His Ser Asp Tyr Lys Val Lys Gly Leu Cys Asp Ser
 180 185 190 195
 AAC CTC ATT TCC ATG GAC ATC ACC TTC TTC TCA GAG GAC GGA GAG CTA 4406
 Asn Leu Ile Ser Met Asp Ile Thr Phe Phe Ser Glu Asp Gly Glu Leu
 200 205 210
 TCA TCC CTG GGA AAG GAG GGC ACA GGG TTC AGA AGT AAC TAC TTT GCT 4454
 Ser Ser Leu Gly Lys Glu Gly Thr Gly Phe Arg Ser Asn Tyr Phe Ala

- 78 -

Val Gly Ile His Leu Cys Ile Lys Leu Lys His Thr Lys Lys Arg Gln
485 490 495

ATT TAT ACA GAC ATA GAG ATG AAC CGA CTT GGA AAG TAA CTCAAATCCT 5319
Ile Tyr Thr Asp Ile Glu Met Asn Arg Leu Gly Lys
500 505 510

GCTAGCCAGA TTCTTCATGT TTGGACCAAA TCAACTTGTG ATACCATGCT CAAAGAGGCC 5379

TCAATTATAT TTGAGTTTTT AATTTTTATG AAAAAAACTA ACAGCAATC ATG GAA 5434
Met Glu
1

GTC CAC GAT TTT GAG ACC GAC GAG TTC AAT GAT TTC AAT GAA GAT GAC 5482
Val His Asp Phe Glu Thr Asp Glu Phe Asn Asp Phe Asn Glu Asp Asp
5 10 15

TAT GCC ACA AGA GAA TTC CTG AAT CCC GAT GAG CGC ATG ACG TAC TTG 5530
Tyr Ala Thr Arg Glu Phe Leu Asn Pro Asp Glu Arg Met Thr Tyr Leu
20 25 30

AAT CAT GCT GAT TAC AAT TTG AAT TCT CCT CTA ATT AGT GAT GAT ATT 5578
Asn His Ala Asp Tyr Asn Leu Asn Ser Pro Leu Ile Ser Asp Asp Ile
35 40 45 50

GAC AAT TTG ATC AGG AAA TTC AAT TCT CTT CCG ATT CCC TCG ATG TGG 5626
Asp Asn Leu Ile Arg Lys Phe Asn Ser Leu Pro Ile Pro Ser Met Trp
55 60 65

GAT AGT AAG AAC TGG GAT GGA GTT CTT GAG ATG TTA ACA TCA TGT CAA 5674
Asp Ser Lys Asn Trp Asp Gly Val Leu Glu Met Leu Thr Ser Cys Gln
70 75 80

GCC AAT CCC ATC TCA ACA TCT CAG ATG CAT AAA TGC ATG GGA AGT TGG 5722
Ala Asn Pro Ile Ser Thr Ser Gln Met His Lys Trp Met Gly Ser Trp
85 90 95

TTA ATG TCT GAT AAT CAT GAT GCC AGT CAA GGG TAT AGT TTT TTA CAT 5770
Leu Met Ser Asp Asn His Asp Ala Ser Gln Gly Tyr Ser Phe Leu His
100 105 110

GAA GTG GAC AAA GAG GCA GAA ATA ACA TTT GAC GTG GTG GAG ACC TTC 5818
Glu Val Asp Lys Glu Ala Glu Ile Thr Phe Asp Val Val Glu Thr Phe
115 120 125 130

ATC CGC GGC TGG GGC AAC AAA CCA ATT GAA TAC ATC AAA AAG GAA AGA 5866
Ile Arg Gly Trp Gly Asn Lys Pro Ile Glu Tyr Ile Lys Lys Glu Arg
135 140 145

TGG ACT GAC TCA TTC AAA ATT CTC GCT TAT TTG TGT CAA AAG TTT TTG 5914
Trp Thr Asp Ser Phe Lys Ile Leu Ala Tyr Leu Cys Gln Lys Phe Leu
150 155 160

GAC TTA CAC AAG TTG ACA TTA ATC TTA AAT GCT GTC TCT GAG GTG GAA 5962
Asp Leu His Lys Leu Thr Leu Ile Leu Asn Ala Val Ser Glu Val Glu
165 170 175

TTG CTC AAC TTG GCG AGG ACT TTC AAA GGC AAA GTC AGA AGA AGT TCT 6010
Leu Leu Asn Leu Ala Arg Thr Phe Lys Gly Lys Val Arg Arg Ser Ser
180 185 190

CAT GGA ACG AAC ATA TGC AGG ATT AGG GTT CCC AGC TTG GGT CCT ACT 6058
His Gly Thr Asn Ile Cys Arg Ile Arg Val Pro Ser Leu Gly Pro Thr
195 200 205 210

TTT ATT TCA GAA GGA TGG GCT TAC TTC AAG AAA CTT GAT ATT CTA ATG 6106
Phe Ile Ser Glu Gly Trp Ala Tyr Phe Lys Lys Leu Asp Ile Leu Met

	215	220	225	
GAC CGA AAC TTT CTG TTA ATG GTC AAA GAT GTG ATT ATA GGG AGG ATG				6154
Asp Arg Asn Phe Leu Leu Met Val Lys Asp Val Ile Ile Gly Arg Met				
	230	235	240	
CAA ACG GTG CTA TCC ATG GTA TGT AGA ATA GAC AAC CTG TTC TCA GAG				6202
Gln Thr Val Leu Ser Met Val Cys Arg Ile Asp Asn Leu Phe Ser Glu				
	245	250	255	
CAA GAC ATC TTC TCC CTT CTA AAT ATC TAC AGA ATT GGA GAT AAA ATT				6250
Gln Asp Ile Phe Ser Leu Leu Asn Ile Tyr Arg Ile Gly Asp Lys Ile				
	260	265	270	
GTG GAG AGG CAG GGA AAT TTT TCT TAT GAC TTG ATT AAA ATG GTG GAA				6298
Val Glu Arg Gln Gly Asn Phe Ser Tyr Asp Leu Ile Lys Met Val Glu				
	275	280	285	290
CCG ATA TGC AAC TTG AAG CTG ATG AAA TTA GCA AGA GAA TCA AGG CCT				6346
Pro Ile Cys Asn Leu Lys Leu Met Lys Leu Ala Arg Glu Ser Arg Pro				
	295	300	305	
TTA GTC CCA CAA TTC CCT CAT TTT GAA AAT CAT ATC AAG ACT TCT GTT				6394
Leu Val Pro Gln Phe Pro His Phe Glu Asn His Ile Lys Thr Ser Val				
	310	315	320	
GAT GAA GGG GCA AAA ATT GAC CGA GGT ATA AGA TTC CTC CAT GAT CAG				6442
Asp Glu Gly Ala Lys Ile Asp Arg Gly Ile Arg Phe Leu His Asp Gln				
	325	330	335	
ATA ATG AGT GTG AAA ACA GTG GAT CTC ACA CTG GTG ATT TAT GGA TCG				6490
Ile Met Ser Val Lys Thr Val Asp Leu Thr Leu Val Ile Tyr Gly Ser				
	340	345	350	
TTC AGA CAT TGG GGT CAT CCT TTT ATA GAT TAT TAC ACT GGA CTA GAA				6538
Phe Arg His Trp Gly His Pro Phe Ile Asp Tyr Tyr Thr Gly Leu Glu				
	355	360	365	370
AAA TTA CAT TCC CAA GTA ACC ATG AAG AAA GAT ATT GAT GTG TCA TAT				6586
Lys Leu His Ser Gln Val Thr Met Lys Lys Asp Ile Asp Val Ser Tyr				
	375	380	385	
GCA AAA GCA CTT GCA AGT GAT TTA GCT CGG ATT GTT CTA TTT CAA CAG				6634
Ala Lys Ala Leu Ala Ser Asp Leu Ala Arg Ile Val Leu Phe Gln Gln				
	390	395	400	
TTC AAT GAT CAT AAA AAG TGG TTC GTG AAT GGA GAC TTG CTC CCT CAT				6682
Phe Asn Asp His Lys Lys Trp Phe Val Asn Gly Asp Leu Leu Pro His				
	405	410	415	
GAT CAT CCC TTT AAA AGT CAT GTT AAA GAA AAT ACA TGG CCC ACA GCT				6730
Asp His Pro Phe Lys Ser His Val Lys Glu Asn Thr Trp Pro Thr Ala				
	420	425	430	
GCT CAA GTT CAA GAT TTT GGA GAT AAA TGG CAT GAA CTT CCG CTG ATT				6778
Ala Gln Val Gln Asp Phe Gly Asp Lys Trp His Glu Leu Pro Leu Ile				
	435	440	445	450
AAA TGT TTT GAA ATA CCC GAC TTA CTA GAC CCA TCG ATA ATA TAC TCT				6826
Lys Cys Phe Glu Ile Pro Asp Leu Leu Asp Pro Ser Ile Ile Tyr Ser				
	455	460	465	
GAC AAA AGT CAT TCA ATG AAT AGG TCA GAG GTG TTG AAA CAT GTC CGA				6874
Asp Lys Ser His Ser Met Asn Arg Ser Glu Val Leu Lys His Val Arg				
	470	475	480	
ATG AAT CCG AAC ACT CCT ATC CCT AGT AAA AAG GTG TTG CAG ACT ATG				6922

Met	Asn	Pro	Asn	Thr	Pro	Ile	Pro	Ser	Lys	Lys	Val	Leu	Gln	Thr	Met	
	485						490					495				
TTG	GAC	ACA	AAG	GCT	ACC	AAT	TGG	AAA	GAA	TTT	CTT	AAA	GAG	ATT	GAT	6970
Leu	Asp	Thr	Lys	Ala	Thr	Asn	Trp	Lys	Glu	Phe	Leu	Lys	Glu	Ile	Asp	
	500					505					510					
GAG	AAG	GGC	TTA	GAT	GAT	GAT	GAT	CTA	ATT	ATT	GGT	CTT	AAA	GGA	AAG	7018
Glu	Lys	Gly	Leu	Asp	Asp	Asp	Asp	Leu	Ile	Ile	Gly	Leu	Lys	Gly	Lys	
	515				520					525					530	
GAG	AGG	GAA	CTG	AAG	TTG	GCA	GGT	AGA	TTT	TTC	TCC	CTA	ATG	TCT	TGG	7066
Glu	Arg	Glu	Leu	Lys	Leu	Ala	Gly	Arg	Phe	Phe	Ser	Leu	Met	Ser	Trp	
				535					540					545		
AAA	TTG	CGA	GAA	TAC	TTT	GTA	ATT	ACC	GAA	TAT	TTG	ATA	AAG	ACT	CAT	7114
Lys	Leu	Arg	Glu	Tyr	Phe	Val	Ile	Thr	Glu	Tyr	Leu	Ile	Lys	Thr	His	
			550					555					560			
TTC	GTC	CCT	ATG	TTT	AAA	GGC	CTG	ACA	ATG	GCG	GAC	GAT	CTA	ACT	GCA	7162
Phe	Val	Pro	Met	Phe	Lys	Gly	Leu	Thr	Met	Ala	Asp	Asp	Leu	Thr	Ala	
		565					570					575				
GTC	ATT	AAA	AAG	ATG	TTA	GAT	TCC	TCA	TCC	GGC	CAA	GGA	TTG	AAG	TCA	7210
Val	Ile	Lys	Lys	Met	Leu	Asp	Ser	Ser	Ser	Gly	Gln	Gly	Leu	Lys	Ser	
	580					585					590					
TAT	GAG	GCA	ATT	TGC	ATA	GCC	AAT	CAC	ATT	GAT	TAC	GAA	AAA	TGG	AAT	7258
Tyr	Glu	Ala	Ile	Cys	Ile	Ala	Asn	His	Ile	Asp	Tyr	Glu	Lys	Trp	Asn	
	595				600					605					610	
AAC	CAC	CAA	AGG	AAG	TTA	TCA	AAC	GGC	CCA	GTG	TTC	CGA	GTT	ATG	GGC	7306
Asn	His	Gln	Arg	Lys	Leu	Ser	Asn	Gly	Pro	Val	Phe	Arg	Val	Met	Gly	
				615					620					625		
CAG	TTC	TTA	GGT	TAT	CCA	TCC	TTA	ATC	GAG	AGA	ACT	CAT	GAA	TTT	TTT	7354
Gln	Phe	Leu	Gly	Tyr	Pro	Ser	Leu	Ile	Glu	Arg	Thr	His	Glu	Phe	Phe	
			630					635					640			
GAG	AAA	AGT	CTT	ATA	TAC	TAC	AAT	GGA	AGA	CCA	GAC	TTG	ATG	CGT	GTT	7402
Glu	Lys	Ser	Leu	Ile	Tyr	Tyr	Asn	Gly	Arg	Pro	Asp	Leu	Met	Arg	Val	
		645					650					655				
CAC	AAC	AAC	ACA	CTG	ATC	AAT	TCA	ACC	TCC	CAA	CGA	GTT	TGT	TGG	CAA	7450
His	Asn	Asn	Thr	Leu	Ile	Asn	Ser	Thr	Ser	Gln	Arg	Val	Cys	Trp	Gln	
		660				665					670					
GGA	CAA	GAG	GGT	GGA	CTG	GAA	GGT	CTA	CGG	CAA	AAA	GGA	TGG	ACT	ATC	7498
Gly	Gln	Glu	Gly	Gly	Leu	Glu	Gly	Leu	Arg	Gln	Lys	Gly	Trp	Thr	Ile	
					680				685						690	
CTC	AAT	CTA	CTG	GTT	ATT	CAA	AGA	GAG	GCT	AAA	ATC	AGA	AAC	ACT	GCT	7546
Leu	Asn	Leu	Leu	Val	Ile	Gln	Arg	Glu	Ala	Lys	Ile	Arg	Asn	Thr	Ala	
				695				700						705		
GTC	AAA	GTC	TTG	GCA	CAA	GGT	GAT	AAT	CAA	GTT	ATT	TGC	ACA	CAG	TAT	7594
Val	Lys	Val	Leu	Ala	Gln	Gly	Asp	Asn	Gln	Val	Ile	Cys	Thr	Gln	Tyr	
			710					715					720			
AAA	ACG	AAG	AAA	TCG	AGA	AAC	GTT	GTA	GAA	TTA	CAG	GGT	GCT	CTC	AAT	7642
Lys	Thr	Lys	Lys	Ser	Arg	Asn	Val	Val	Glu	Leu	Gln	Gly	Ala	Leu	Asn	
		725					730					735				
CAA	ATG	GTT	TCT	AAT	AAT	GAG	AAA	ATT	ATG	ACT	GCA	ATC	AAA	ATA	GGG	7690
Gln	Met	Val	Ser	Asn	Asn	Glu	Lys	Ile	Met	Thr	Ala	Ile	Lys	Ile	Gly	
	740					745						750				

ACA GGG AAG TTA GGA CTT TTG ATA AAT GAC GAT GAG ACT ATG CAA TCT Thr Gly Lys Leu Gly Leu Leu Ile Asn Asp Asp Glu Thr Met Gln Ser 755 760 765 770	7738
GCA GAT TAC TTG AAT TAT GGA AAA ATA CCG ATT TTC CGT GGA GTG ATT Ala Asp Tyr Leu Asn Tyr Gly Lys Ile Pro Ile Phe Arg Gly Val Ile 775 780 785	7786
AGA GGG TTA GAG ACC AAG AGA TGG TCA CGA GTG ACT TGT GTC ACC AAT Arg Gly Leu Glu Thr Lys Arg Trp Ser Arg Val Thr Cys Val Thr Asn 790 795 800	7834
GAC CAA ATA CCC ACT TGT GCT AAT ATA ATG AGC TCA GTT TCC ACA AAT Asp Gln Ile Pro Thr Cys Ala Asn Ile Met Ser Ser Val Ser Thr Asn 805 810 815	7882
GCT CTC ACC GTA GCT CAT TTT GCT GAG AAC CCA ATC AAT GCC ATG ATA Ala Leu Thr Val Ala His Phe Ala Glu Asn Pro Ile Asn Ala Met Ile 820 825 830	7930
CAG TAC AAT TAT TTT GGG ACA TTT GCT AGA CTC TTG TTG ATG ATG CAT Gln Tyr Asn Tyr Phe Gly Thr Phe Ala Arg Leu Leu Met Met His 835 840 845 850	7978
GAT CCT GCT CTT CGT CAA TCA TTG TAT GAA GTT CAA GAT AAG ATA CCG Asp Pro Ala Leu Arg Gln Ser Leu Tyr Glu Val Gln Asp Lys Ile Pro 855 860 865	8026
GGC TTG CAC AGT TCT ACT TTC AAA TAC GCC ATG TTG TAT TTG GAC CCT Gly Leu His Ser Ser Thr Phe Lys Tyr Ala Met Leu Tyr Leu Asp Pro 870 875 880	8074
TCC ATT GGA GGA GTG TCG GGC ATG TCT TTG TCC AGG TTT TTG ATT AGA Ser Ile Gly Gly Val Ser Gly Met Ser Leu Ser Arg Phe Leu Ile Arg 885 890 895	8122
GCC TTC CCA GAT CCC GTA ACA GAA AGT CTC TCA TTC TGG AGA TTC ATC Ala Phe Pro Asp Pro Val Thr Glu Ser Leu Ser Phe Trp Arg Phe Ile 900 905 910	8170
CAT GTA CAT GCT CGA AGT GAG CAT CTG AAG GAG ATG AGT GCA GTA TTT His Val His Ala Arg Ser Glu His Leu Lys Glu Met Ser Ala Val Phe 915 920 925 930	8218
GGA AAC CCC GAG ATA GCC AAG TTT CGA ATA ACT CAC ATA GAC AAG CTA Gly Asn Pro Glu Ile Ala Lys Phe Arg Ile Thr His Ile Asp Lys Leu 935 940 945	8266
GTA GAA GAT CCA ACC TCT CTG AAC ATC GCT ATG GGA ATG AGT CCA GCG Val Glu Asp Pro Thr Ser Leu Asn Ile Ala Met Gly Met Ser Pro Ala 950 955 960	8314
AAC TTG TTA AAG ACT GAG GTT AAA AAA TGC TTA ATC GAA TCA AGA CAA Asn Leu Leu Lys Thr Glu Val Lys Lys Cys Leu Ile Glu Ser Arg Gln 965 970 975	8362
ACC ATC AGG AAC CAG GTG ATT AAG GAT GCA ACC ATA TAT TTG TAT CAT Thr Ile Arg Asn Gln Val Ile Lys Asp Ala Thr Ile Tyr Leu Tyr His 980 985 990	8410
GAA GAG GAT CGG CTC AGA AGT TTC TTA TGG TCA ATA AAT CCT CTG TTC Glu Glu Asp Arg Leu Arg Ser Phe Leu Trp Ser Ile Asn Pro Leu Phe 995 1000 1005 1010	8458
CCT AGA TTT TTA AGT GAA TTC AAA TCA GGC ACT TTT TTG GGA GTC GCA Pro Arg Phe Leu Ser Glu Phe Lys Ser Gly Thr Phe Leu Gly Val Ala 1015 1020 1025	8506

GAC GGG CTC ATC AGT CTA TTT CAA AAT TCT CGT ACT ATT CGG AAC TCC Asp Gly Leu Ile Ser Leu Phe Gln Asn Ser Arg Thr Ile Arg Asn Ser 1030 1035 1040	8554
TTT AAG AAA AAG TAT CAT AGG GAA TTG GAT GAT TTG ATT GTG AGG AGT Phe Lys Lys Lys Tyr His Arg Glu Leu Asp Asp Leu Ile Val Arg Ser 1045 1050 1055	8602
GAG GTA TCC TCT TTG ACA CAT TTA GGG AAA CTT CAT TTG AGA AGG GGA Glu Val Ser Ser Leu Thr His Leu Gly Lys Leu His Leu Arg Arg Gly 1060 1065 1070	8650
TCA TGT AAA ATG TGG ACA TGT TCA GCT ACT CAT GCT GAC ACA TTA AGA Ser Cys Lys Met Trp Thr Cys Ser Ala Thr His Ala Asp Thr Leu Arg 1075 1080 1085 1090	8698
TAC AAA TCC TGG GGC CGT ACA GTT ATT GGG ACA ACT GTA CCC CAT CCA Tyr Lys Ser Trp Gly Arg Thr Val Ile Gly Thr Thr Val Pro His Pro 1095 1100 1105	8746
TTA GAA ATG TTG GGT CCA CAA CAT CGA AAA GAG ACT CCT TGT GCA CCA Leu Glu Met Leu Gly Pro Gln His Arg Lys Glu Thr Pro Cys Ala Pro 1110 1115 1120	8794
TGT AAC ACA TCA GGG TTC AAT TAT GTT TCT GTG CAT TGT CCA GAC GGG Cys Asn Thr Ser Gly Phe Asn Tyr Val Ser Val His Cys Pro Asp Gly 1125 1130 1135	8842
ATC CAT GAC GTC TTT AGT TCA CGG GGA CCA TTG CCT GCT TAT CTA GGG Ile His Asp Val Phe Ser Ser Arg Gly Pro Leu Pro Ala Tyr Leu Gly 1140 1145 1150	8890
TCT AAA ACA TCT GAA TCT ACA TCT ATT TTG CAG CCT TGG GAA AGG GAA Ser Lys Thr Ser Glu Ser Thr Ser Ile Leu Gln Pro Trp Glu Arg Glu 1155 1160 1165 1170	8938
AGC AAA GTC CCA CTG ATT AAA AGA GCT ACA CGT CTT AGA GAT GCT ATC Ser Lys Val Pro Leu Ile Lys Arg Ala Thr Arg Leu Arg Asp Ala Ile 1175 1180 1185	8986
TCT TGG TTT GTT GAA CCC GAC TCT AAA CTA GCA ATG ACT ATA CTT TCT Ser Trp Phe Val Glu Pro Asp Ser Lys Leu Ala Met Thr Ile Leu Ser 1190 1195 1200	9034
AAC ATC CAC TCT TTA ACA GGC GAA GAA TGG ACC AAA AGG CAG CAT GGG Asn Ile His Ser Leu Thr Gly Glu Glu Trp Thr Lys Arg Gln His Gly 1205 1210 1215	9082
TTC AAA AGA ACA GGG TCT GCC CTT CAT AGG TTT TCG ACA TCT CGG ATG Phe Lys Arg Thr Gly Ser Ala Leu His Arg Phe Ser Thr Ser Arg Met 1220 1225 1230	9130
AGC CAT GGT GGG TTC GCA TCT CAG AGC ACT GCA GCA TTG ACC AGG TTG Ser His Gly Gly Phe Ala Ser Gln Ser Thr Ala Ala Leu Thr Arg Leu 1235 1240 1245 1250	9178
ATG GCA ACT ACA GAC ACC ATG AGG GAT CTG GGA GAT CAG AAT TTC GAC Met Ala Thr Thr Asp Thr Met Arg Asp Leu Gly Asp Gln Asn Phe Asp 1255 1260 1265	9226
TTT TTA TTC CAA GCA ACG TTG CTC TAT GCT CAA ATT ACC ACC ACT GTT Phe Leu Phe Gln Ala Thr Leu Leu Tyr Ala Gln Ile Thr Thr Thr Val 1270 1275 1280	9274
GCA AGA GAC GGA TGG ATC ACC AGT TGT ACA GAT CAT TAT CAT ATT GCC Ala Arg Asp Gly Trp Ile Thr Ser Cys Thr Asp His Tyr His Ile Ala 1285 1290 1295	9322

TGT AAG TCC TGT TTG AGA CCC ATA GAA GAG ATC ACC CTG GAC TCA AGT Cys Lys Ser Cys Leu Arg Pro Ile Glu Glu Ile Thr Leu Asp Ser Ser 1300 1305 1310	9370
ATG GAC TAC ACG CCC CCA GAT GTA TCC CAT GTG CTG AAG ACA TGG AGG Met Asp Tyr Thr Pro Pro Asp Val Ser His Val Leu Lys Thr Trp Arg 1315 1320 1325 1330	9418
AAT GGG GAA GGT TCG TGG GGA CAA GAG ATA AAA CAG ATC TAT CCT TTA Asn Gly Glu Gly Ser Trp Gly Gln Glu Ile Lys Gln Ile Tyr Pro Leu 1335 1340 1345	9466
GAA GGG AAT TGG AAG AAT TTA GCA CCT GCT GAG CAA TCC TAT CAA GTC Glu Gly Asn Trp Lys Asn Leu Ala Pro Ala Glu Gln Ser Tyr Gln Val 1350 1355 1360	9514
GGC AGA TGT ATA GGT TTT CTA TAT GGA GAC TTG GCG TAT AGA AAA TCT Gly Arg Cys Ile Gly Phe Leu Tyr Gly Asp Leu Ala Tyr Arg Lys Ser 1365 1370 1375	9562
ACT CAT GCC GAG GAC AGT TCT CTA TTT CCT CTA TCT ATA CAA GGT CGT Thr His Ala Glu Asp Ser Ser Leu Phe Pro Leu Ser Ile Gln Gly Arg 1380 1385 1390	9610
ATT AGA GGT CGA GGT TTC TTA AAA GGG TTG CTA GAC GGA TTA ATG AGA Ile Arg Gly Arg Gly Phe Leu Lys Gly Leu Leu Asp Gly Leu Met Arg 1395 1400 1405 1410	9658
GCA AGT TGC TGC CAA GTA ATA CAC CGG AGA AGT CTG GCT CAT TTG AAG Ala Ser Cys Cys Gln Val Ile His Arg Arg Ser Leu Ala His Leu Lys 1415 1420 1425	9706
AGG CCG GCC AAC GCA GTG TAC GGA GGT TTG ATT TAC TTG ATT GAT AAA Arg Pro Ala Asn Ala Val Tyr Gly Gly Leu Ile Thr Leu Ile Asp Lys 1430 1435 1440	9754
TTG AGT GTA TCA CCT CCA TTC CTT TCT CTT ACT AGA TCA GGA CCT ATT Leu Ser Val Ser Pro Pro Phe Leu Ser Leu Thr Arg Ser Gly Pro Ile 1445 1450 1455	9802
AGA GAC GAA TTA GAA ACG ATT CCC CAC AAG ATC CCA ACC TCC TAT CCG Arg Asp Glu Leu Glu Thr Ile Pro His Lys Ile Pro Thr Ser Tyr Pro 1460 1465 1470	9850
ACA AGC AAC CGT GAT ATG GGG GTG ATT GTC AGA AAT TAC TTC AAA TAC Thr Ser Asn Arg Asp Met Gly Val Ile Val Arg Asn Tyr Phe Lys Tyr 1475 1480 1485 1490	9898
CAA TGC CGT CTA ATT GAA AAG GGA AAA TAC AGA TCA CAT TAT TCA CAA Gln Cys Arg Leu Ile Glu Lys Gly Lys Tyr Arg Ser His Tyr Ser Gln 1495 1500 1505	9946
TTA TGG TTA TTC TCA GAT GTC TTA TCC ATA GAC TTC ATT GGA CCA TTC Leu Trp Leu Phe Ser Asp Val Leu Ser Ile Asp Phe Ile Gly Pro Phe 1510 1515 1520	9994
TCT ATT TCC ACC ACC CTC TTG CAA ATC CTA TAC AAG CCA TTT TTA TCT Ser Ile Ser Thr Thr Leu Leu Gln Ile Leu Tyr Lys Pro Phe Leu Ser 1525 1530 1535	10042
GGG AAA GAT AAG AAT GAG TTG AGA GAG CTG GCA AAT CTT TCT TCA TTG Gly Lys Asp Lys Asn Glu Leu Arg Glu Leu Ala Asn Leu Ser Ser Leu 1540 1545 1550	10090
CTA AGA TCA GGA GAG GGG TGG GAA GAC ATA CAT GTG AAA TTC TTC ACC Leu Arg Ser Gly Glu Gly Trp Glu Asp Ile His Val Lys Phe Phe Thr 1555 1560 1565 1570	10138

AAG GAC ATA TTA TTG TGT CCA GAG GAA ATC AGA CAT GCT TGC AAG TTC Lys Asp Ile Leu Leu Cys Pro Glu Glu Ile Arg His Ala Cys Lys Phe 1575 1580 1585	10186
GGG ATT GCT AAG GAT AAT AAT AAA GAC ATG AGC TAT CCC CCT TGG GGA Gly Ile Ala Lys Asp Asn Asn Lys Asp Met Ser Tyr Pro Pro Trp Gly 1590 1595 1600	10234
AGG GAA TCC AGA GGG ACA ATT ACA ACA ATC CCT GTT TAT TAT ACG ACC Arg Glu Ser Arg Gly Thr Ile Thr Thr Ile Pro Val Tyr Tyr Thr Thr 1605 1610 1615	10282
ACC CCT TAC CCA AAG ATG CTA GAG ATG CCT CCA AGA ATC CAA AAT CCC Thr Pro Tyr Pro Lys Met Leu Glu Met Pro Pro Arg Ile Gln Asn Pro 1620 1625 1630	10330
CTG CTG TCC GGA ATC AGG TTG GGC CAA TTA CCA ACT GGC GCT CAT TAT Leu Leu Ser Gly Ile Arg Leu Gly Gln Leu Pro Thr Gly Ala His Tyr 1635 1640 1645 1650	10378
AAA ATT CGG AGT ATA TTA CAT GGA ATG GGA ATC CAT TAC AGG GAC TTC Lys Ile Arg Ser Ile Leu His Gly Met Gly Ile His Tyr Arg Asp Phe 1655 1660 1665	10426
TTG AGT TGT GGA GAC GGC TCC GGA GGG ATG ACT GCT GCA TTA CTA CGA Leu Ser Cys Gly Asp Gly Ser Gly Gly Met Thr Ala Ala Leu Leu Arg 1670 1675 1680	10474
GAA AAT GTG CAT AGC AGA GGA ATA TTC AAT AGT CTG TTA GAA TTA TCA Glu Asn Val His Ser Arg Gly Ile Phe Asn Ser Leu Leu Glu Leu Ser 1685 1690 1695	10522
GGG TCA GTC ATG CGA GGC GCC TCT CCT GAG CCC CCC AGT GCC CTA GAA Gly Ser Val Met Arg Gly Ala Ser Pro Glu Pro Pro Ser Ala Leu Glu 1700 1705 1710	10570
ACT TTA GGA GGA GAT AAA TCG AGA TGT GTA AAT GGT GAA ACA TGT TGG Thr Leu Gly Gly Asp Lys Ser Arg Cys Val Asn Gly Glu Thr Cys Trp 1715 1720 1725 1730	10618
GAA TAT CCA TCT GAC TTA TGT GAC CCA AGG ACT TGG GAC TAT TTC CTC Glu Tyr Pro Ser Asp Leu Cys Asp Pro Arg Thr Trp Asp Tyr Phe Leu 1735 1740 1745	10666
CGA CTC AAA GCA GGC TTG GGG CTT CAA ATT GAT TTA ATT GTA ATG GAT Arg Leu Lys Ala Gly Leu Gly Leu Gln Ile Asp Leu Ile Val Met Asp 1750 1755 1760	10714
ATG GAA GTT CGG GAT TCT TCT ACT AGC CTG AAA ATT GAG ACG AAT GTT Met Glu Val Arg Asp Ser Ser Thr Ser Leu Lys Ile Glu Thr Asn Val 1765 1770 1775	10762
AGA AAT TAT GTG CAC CGG ATT TTG GAT GAG CAA GGA GTT TTA ATC TAC Arg Asn Tyr Val His Arg Ile Leu Asp Glu Gln Gly Val Leu Ile Tyr 1780 1785 1790	10810
AAG ACT TAT GGA ACA TAT ATT TGT GAG AGC GAA AAG AAT GCA GTA ACA Lys Thr Tyr Gly Thr Tyr Ile Cys Glu Ser Glu Lys Asn Ala Val Thr 1795 1800 1805 1810	10858
ATC CTT GGT CCC ATG TTC AAG ACG GTC GAC TTA GTT CAA ACA GAA TTT Ile Leu Gly Pro Met Phe Lys Thr Val Asp Leu Val Gln Thr Glu Phe 1815 1820 1825	10906
AGT AGT TCT CAA ACG TCT GAA GTA TAT ATG GTA TGT AAA GGT TTG AAG Ser Ser Ser Gln Thr Ser Glu Val Tyr Met Val Cys Lys Gly Leu Lys 1830 1835 1840	10954

AAA TTA ATC GAT GAA CCC AAT CCC GAT TGG TCT TCC ATC AAT GAA TCC Lys Leu Ile Asp Glu Pro Asn Pro Asp Trp Ser Ser Ile Asn Glu Ser 1845 1850 1855	11002
TGG AAA AAC CTG TAC GCA TTC CAG TCA TCA GAA CAG GAA TTT GCC AGA Trp Lys Asn Leu Tyr Ala Phe Gln Ser Ser Glu Gln Glu Phe Ala Arg 1860 1865 1870	11050
GCA AAG AAG GTT AGT ACA TAC TTT ACC TTG ACA GGT ATT CCC TCC CAA Ala Lys Lys Val Ser Thr Tyr Phe Thr Leu Thr Gly Ile Pro Ser Gln 1875 1880 1885 1890	11098
TTC ATT CCT GAT CCT TTT GTA AAC ATT GAG ACT ATG CTA CAA ATA TTC Phe Ile Pro Asp Pro Phe Val Asn Ile Glu Thr Met Leu Gln Ile Phe 1895 1900 1905	11146
GGA GTA CCC ACG GGT GTG TCT CAT GCG GCT GCC TTA AAA TCA TCT GAT Gly Val Pro Thr Gly Val Ser His Ala Ala Ala Leu Lys Ser Ser Asp 1910 1915 1920	11194
AGA CCT GCA GAT TTA TTG ACC ATT AGC CTT TTT TAT ATG GCG ATT ATA Arg Pro Ala Asp Leu Leu Thr Ile Ser Leu Phe Tyr Met Ala Ile Ile 1925 1930 1935	11242
TCG TAT TAT AAC ATC AAT CAT ATC AGA GTA GGA CCG ATA CCT CCG AAC Ser Tyr Tyr Asn Ile Asn His Ile Arg Val Gly Pro Ile Pro Pro Asn 1940 1945 1950	11290
CCC CCA TCA GAT GGA ATT GCA CAA AAT GTG GGG ATC GCT ATA ACT GGT Pro Pro Ser Asp Gly Ile Ala Gln Asn Val Gly Ile Ala Ile Thr Gly 1955 1960 1965 1970	11338
ATA AGC TTT TGG CTG AGT TTG ATG GAG AAA GAC ATT CCA CTA TAT CAA Ile Ser Phe Trp Leu Ser Leu Met Glu Lys Asn Ile Pro Ile Thr Gln 1975 1980 1985	11386
CAG TGT TTA GCA GTT ATC CAG CAA TCA TTC CCG ATT AGG TGG GAG GCT Gln Cys Leu Ala Val Ile Gln Gln Ser Phe Pro Ile Arg Trp Glu Ala 1990 1995 2000	11434
GTT TCA GTA AAA GGA GGA TAC AAG CAG AAG TGG AGT ACT AGA GGT GAT Val Ser Val Lys Gly Gly Tyr Lys Gln Lys Trp Ser Thr Arg Gly Asp 2005 2010 2015	11482
GGG CTC CCA AAA GAT ACC CGA ACT TCA GAC TCC TTG GCC CCA ATC GGG Gly Leu Pro Lys Asp Thr Arg Thr Ser Asp Ser Leu Ala Pro Ile Gly 2020 2025 2030	11530
AAC TGG ATC AGA TCT CTG GAA TTG GTC CGA AAC CAA GTT CGT CTA AAT Asn Trp Ile Arg Ser Leu Glu Leu Val Arg Asn Gln Val Arg Leu Asn 2035 2040 2045 2050	11578
CCA TTC AAT GAG ATC TTG TTC AAT CAG CTA TGT CGT ACA GTG GAT AAT Pro Phe Asn Glu Ile Leu Phe Asn Gln Leu Cys Arg Thr Val Asp Asn 2055 2060 2065	11626
CAT TTG AAA TGG TCA AAT TTG CGA AGA AAC ACA GGA ATG ATT GAA TGG His Leu Lys Trp Ser Asn Leu Arg Arg Asn Thr Gly Met Ile Glu Trp 2070 2075 2080	11674
ATC AAT AGA CGA ATT TCA AAA GAA GAC CGG TCT ATA CTG ATG TTG AAG Ile Asn Arg Arg Ile Ser Lys Glu Asp Arg Ser Ile Leu Met Leu Lys 2085 2090 2095	11722
AGT GAC CTA CAC GAG GAA AAC TCT TGG AGA GAT TAA AAAATCATGA Ser Asp Leu His Glu Glu Asn Ser Trp Arg Asp 2100 2105	11768

GGAGACTCCA AACTTTAAGT ATGAAAAAAA CTTTGATCCT TAAGACCCTC TTGTGGTTTT 11828
TATTTTTTAT CTGGTTTTGT GGTCTTCGTG GGTCGGCATG GCATCTCCAC CTCCTCGCGG 11888
TCCGACCTGG GCATCCGAAG GAGGACGTG TCCACTCGGA TGGCTAAGGG AGGGGCCCCC 11948
GCGGGGCTGC TAACAAAGCC CGAAAGGAAG CTGAGTTGGC TGCTGCCACC GCTGAGCAAT 12008
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GAACTATATC CGGATCGAGA CCTCGATACT AGTGCGGTGG AGCTCCAGCT TTTGTTCCCT 12128
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CTTTCTCCCT TCGGGAAGCG TGGCGTTTTC TCATAGCTCA CGCTGTAGGT ATCTCAGTTC 12788
GGTGTAGGTC GTTGGCTCCA AGCTGGGCTG TGTGCACGAA CCCCCGTT AGCCCGACCG 12848
CTGCGCCTTA TCCGGTAACT ATCGTCTTGA GTCCAACCCG GTAAGACACG ACTTATCGCC 12908
ACTGGCAGCA GCCACTGGTA ACAGGATTAG CAGAGCGAGG TATGTAGGCG GTGCTACAGA 12968
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TCTGCTGAAG CCAGTTACCT TCGGAAAAAG AGTTGGTAGC TCTTGATCCG GCAAACAAAC 13088
CACCGCTGGT AGCGGTGGTT TTTTGTGTTG CAAGCAGCAG ATTACGCGCA GAAAAAAGG 13148
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CCAATGCTTA ATCAGTGAGG CACCTATCTC AGCGATCTGT CTATTTGTT CATCCATAGT 13388
TGCCTGACTC CCCGTCGTGT AGATAACTAC GATACGGGAG GGCTTACCAT CTGGCCCCAG 13448
TGCTGCAATG ATACGCGAG ACCCAGCTC ACCGGCTCCA GATTATCAG CAATAAACCA 13508
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TGTTGCCATT GCTACAGGCA TCGTGGTGTC ACGCTCGTCG TTTGGTATGG CTTTCATTCAG 13688
CTCCGGTTCC CAACGATCAA GGCGAGTTAC ATGATCCCCC ATGTTGTGCA AAAAAGCGGT 13748
TAGCTCCTTC GGTCTCCGA TCGTTGTCAG AAGTAAGTTG GCCGCAGTGT TATCACTCAT 13808

GGTTATGGCA GCACTGCATA ATTCTCTTAC TGTCATGCCA TCCGTAAGAT GCTTTTCTGT 13868
 GACTGGTGAG TACTCAACCA AGTCATTCTG AGAATAGTGT ATGCGGCGAC CGAGTTGCTC 13928
 TTGCCCCGGCG TCAATACGGG ATAATACCGC GCCACATAGC AGAACTTTAA AAGTGCTCAT 13988
 CATTGGAAAA CGTTCTTCGG GCGGAAAACT CTCAAGGATC TTACCGCTGT TGAGATCCAG 14048
 TTCGATGTAA CCCACTCGTG CACCCAACTG ATCTTCAGCA TCTTTTACTT TCACCAGCGT 14108
 TTCTGGGTGA GCAAAAACAG GAAGGCAAAA TGCCGCAAAA AAGGGAATAA GGGCGACACG 14168
 GAAATGTTGA ATACTCATAC TCTTCCTTTT TCAATATTAT TGAAGCATTT ATCAGGGTTA 14228
 TTGTCTCATG AGCGGATACA TATTTGAATG TATTTAGAAA AATAAACAAA TAGGGGTTCC 14288
 GCGCACATTT CCCCAGAAAAG TGC 14311

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 422 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ser Val Thr Val Lys Arg Ile Ile Asp Asn Thr Val Ile Val Pro
 1 5 10 15
 Lys Leu Pro Ala Asn Glu Asp Pro Val Glu Tyr Pro Ala Arg Tyr Phe
 20 25 30
 Arg Lys Ser Lys Glu Ile Pro Leu Tyr Ile Asn Thr Thr Lys Ser Leu
 35 40 45
 Ser Asp Leu Arg Gly Tyr Val Tyr Gln Gly Leu Lys Ser Gly Asn Val
 50 55 60
 Ser Ile Ile His Val Asn Ser Tyr Leu Tyr Gly Ala Leu Lys Asp Ile
 65 70 75 80
 Arg Gly Lys Leu Asp Lys Asp Trp Ser Ser Phe Gly Ile Asn Ile Gly
 85 90 95
 Lys Ala Gly Asp Thr Ile Gly Ile Phe Asp Leu Val Ser Leu Lys Ala
 100 105 110
 Leu Asp Gly Val Leu Pro Asp Gly Val Ser Asp Ala Ser Arg Thr Ser
 115 120 125
 Ala Asp Asp Lys Trp Leu Pro Leu Tyr Leu Leu Gly Leu Tyr Arg Val
 130 135 140
 Gly Arg Thr Gln Met Pro Glu Tyr Arg Lys Lys Leu Met Asp Gly Leu
 145 150 155 160
 Thr Asn Gln Cys Lys Met Ile Asn Glu Gln Phe Glu Pro Leu Val Pro
 165 170 175
 Glu Gly Arg Asp Ile Phe Asp Val Trp Gly Asn Asp Ser Asn Tyr Thr
 180 185 190
 Lys Ile Val Ala Ala Val Asp Met Phe Phe His Met Phe Lys Lys His

195	200	205
Glu Cys Ala Ser Phe Arg Tyr Gly Thr Ile Val Ser Arg Phe Lys Asp 210 215 220		
Cys Ala Ala Leu Ala Thr Phe Gly His Leu Cys Lys Ile Thr Gly Met 225 230 235 240		
Ser Thr Glu Asp Val Thr Thr Trp Ile Leu Asn Arg Glu Val Ala Asp 245 250 255		
Glu Met Val Gln Met Met Leu Pro Gly Gln Glu Ile Asp Lys Ala Asp 260 265 270		
Ser Tyr Met Pro Tyr Leu Ile Asp Phe Gly Leu Ser Ser Lys Ser Pro 275 280 285		
Tyr Ser Ser Val Lys Asn Pro Ala Phe His Phe Trp Gly Gln Leu Thr 290 295 300		
Ala Leu Leu Leu Arg Ser Thr Arg Ala Arg Asn Ala Arg Gln Pro Asp 305 310 315 320		
Asp Ile Glu Tyr Thr Ser Leu Thr Thr Ala Gly Leu Leu Tyr Ala Tyr 325 330 335		
Ala Val Gly Ser Ser Ala Asp Leu Ala Gln Gln Phe Cys Val Gly Asp 340 345 350		
Asn Lys Tyr Thr Pro Asp Asp Ser Thr Gly Gly Leu Thr Thr Asn Ala 355 360 365		
Pro Pro Gln Gly Arg Asp Val Val Glu Trp Leu Gly Trp Phe Glu Asp 370 375 380		
Gln Asn Arg Lys Pro Thr Pro Asp Met Met Gln Tyr Ala Lys Arg Ala 385 390 395 400		
Val Met Ser Leu Gln Gly Leu Arg Glu Lys Thr Ile Gly Lys Tyr Ala 405 410 415		
Lys Ser Glu Phe Asp Lys 420		

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 265 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Asp Asn Leu Thr Lys Val Arg Glu Tyr Leu Lys Ser Tyr Ser Arg 1 5 10 15
Leu Asp Gln Ala Val Gly Glu Ile Asp Glu Ile Glu Ala Gln Arg Ala 20 25 30
Glu Lys Ser Asn Tyr Glu Leu Phe Gln Glu Asp Gly Val Glu Glu His 35 40 45
Thr Lys Pro Ser Tyr Phe Gln Ala Ala Asp Asp Ser Asp Thr Glu Ser 50 55 60

Glu Pro Glu Ile Glu Asp Asn Gln Gly Leu Tyr Ala Pro Asp Pro Glu
 65 70 75 80
 Ala Glu Gln Val Glu Gly Phe Ile Gln Gly Pro Leu Asp Asp Tyr Ala
 85 90 95
 Asp Glu Glu Val Asp Val Val Phe Thr Ser Asp Trp Lys Gln Pro Glu
 100 105 110
 Leu Glu Ser Asp Glu His Gly Lys Thr Leu Arg Leu Thr Ser Pro Glu
 115 120 125
 Gly Leu Ser Gly Glu Gln Lys Ser Gln Trp Leu Ser Thr Ile Lys Ala
 130 135 140
 Val Val Gln Ser Ala Lys Tyr Trp Asn Leu Ala Glu Cys Thr Phe Glu
 145 150 155 160
 Ala Ser Gly Glu Gly Val Ile Met Lys Glu Arg Gln Ile Thr Pro Asp
 165 170 175
 Val Tyr Lys Val Thr Pro Val Met Asn Thr His Pro Ser Gln Ser Glu
 180 185 190
 Ala Val Ser Asp Val Trp Ser Leu Ser Lys Thr Ser Met Thr Phe Gln
 195 200 205
 Pro Lys Lys Ala Ser Leu Gln Pro Leu Thr Ile Ser Leu Asp Glu Leu
 210 215 220
 Phe Ser Ser Arg Gly Glu Phe Ile Ser Val Gly Gly Asp Gly Arg Met
 225 230 235 240
 Ser His Lys Glu Ala Ile Leu Leu Gly Leu Arg Tyr Lys Lys Leu Tyr
 245 250 255
 Asn Gln Ala Arg Val Lys Tyr Ser Leu
 260 265

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ser Ser Leu Lys Lys Ile Leu Gly Leu Lys Gly Lys Lys Lys
 1 5 10 15
 Ser Lys Lys Leu Gly Ile Ala Pro Pro Pro Tyr Glu Glu Asp Thr Ser
 20 25 30
 Met Glu Tyr Ala Pro Ser Ala Pro Ile Asp Lys Ser Tyr Phe Gly Val
 35 40 45
 Asp Glu Met Asp Thr Tyr Asp Pro Asn Gln Leu Arg Tyr Glu Lys Phe
 50 55 60
 Phe Phe Thr Val Lys Met Thr Val Arg Ser Asn Arg Pro Phe Arg Thr
 65 70 75 80
 Tyr Ser Asp Val Ala Ala Ala Val Ser His Trp Asp His Met Tyr Ile

85 90 95

Gly Met Ala Gly Lys Arg Pro Phe Tyr Lys Ile Leu Ala Phe Leu Gly
100 105 110

Ser Ser Asn Leu Lys Ala Thr Pro Ala Val Leu Ala Asp Gln Gly Gln
115 120 125

Pro Glu Tyr His Thr His Cys Glu Gly Arg Ala Tyr Leu Pro His Arg
130 135 140

Met Gly Lys Thr Pro Pro Met Leu Asn Val Pro Glu His Phe Arg Arg
145 150 155 160

Pro Phe Asn Ile Gly Leu Tyr Lys Gly Thr Ile Glu Leu Thr Met Thr
165 170 175

Ile Tyr Asp Asp Glu Ser Leu Glu Ala Ala Pro Met Ile Trp Asp His
180 185 190

Phe Asn Ser Ser Lys Phe Ser Asp Phe Arg Glu Lys Ala Leu Met Phe
195 200 205

Gly Leu Ile Val Glu Lys Lys Ala Ser Gly Ala Trp Val Leu Asp Ser
210 215 220

Ile Ser His Phe Lys
225

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 511 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Lys Cys Leu Leu Tyr Leu Ala Phe Leu Phe Ile Gly Val Asn Cys
1 5 10 15

Lys Phe Thr Ile Val Phe Pro His Asn Gln Lys Gly Asn Trp Lys Asn
20 25 30

Val Pro Ser Asn Tyr His Tyr Cys Pro Ser Ser Ser Asp Leu Asn Trp
35 40 45

His Asn Asp Leu Ile Gly Thr Ala Ile Gln Val Lys Met Pro Lys Ser
50 55 60

His Lys Ala Ile Gln Ala Asp Gly Trp Met Cys His Ala Ser Lys Trp
65 70 75 80

Val Thr Thr Cys Asp Phe Arg Trp Tyr Gly Pro Lys Tyr Ile Thr Gln
85 90 95

Ser Ile Arg Ser Phe Thr Pro Ser Val Glu Gln Cys Lys Glu Ser Ile
100 105 110

Glu Gln Thr Lys Gln Gly Thr Trp Leu Asn Pro Gly Phe Pro Pro Gln
115 120 125

Ser Cys Gly Tyr Ala Thr Val Thr Asp Ala Glu Ala Val Ile Val Gln
130 135 140

Val Thr Pro His His Val Leu Val Asp Glu Tyr Thr Gly Glu Trp Val
 145 150 155 160
 Asp Ser Gln Phe Ile Asn Gly Lys Cys Ser Asn Tyr Ile Cys Pro Thr
 165 170 175
 Val His Asn Ser Thr Thr Trp His Ser Asp Tyr Lys Val Lys Gly Leu
 180 185 190
 Cys Asp Ser Asn Leu Ile Ser Met Asp Ile Thr Phe Phe Ser Glu Asp
 195 200 205
 Gly Glu Leu Ser Ser Leu Gly Lys Glu Gly Thr Gly Phe Arg Ser Asn
 210 215 220
 Tyr Phe Ala Tyr Glu Thr Gly Gly Lys Ala Cys Lys Met Gln Tyr Cys
 225 230 235 240
 Lys His Trp Gly Val Arg Leu Pro Ser Gly Val Trp Phe Glu Met Ala
 245 250 255
 Asp Lys Asp Leu Phe Ala Ala Ala Arg Phe Pro Glu Cys Pro Glu Gly
 260 265 270
 Ser Ser Ile Ser Ala Pro Ser Gln Thr Ser Val Asp Val Ser Leu Ile
 275 280 285
 Gln Asp Val Glu Arg Ile Leu Asp Tyr Ser Leu Cys Gln Glu Thr Trp
 290 295 300
 Ser Lys Ile Arg Ala Gly Leu Pro Ile Ser Pro Val Asp Leu Ser Tyr
 305 310 315 320
 Leu Ala Pro Lys Asn Pro Gly Thr Gly Pro Ala Phe Thr Ile Ile Asn
 325 330 335
 Gly Thr Leu Lys Tyr Phe Glu Thr Arg Tyr Ile Arg Val Asp Ile Ala
 340 345 350
 Ala Pro Ile Leu Ser Arg Met Val Gly Met Ile Ser Gly Thr Thr Thr
 355 360 365
 Glu Arg Glu Leu Trp Asp Asp Trp Ala Pro Tyr Glu Asp Val Glu Ile
 370 375 380
 Gly Pro Asn Gly Val Leu Arg Thr Ser Ser Gly Tyr Lys Phe Pro Leu
 385 390 395 400
 Tyr Met Ile Gly His Gly Met Leu Asp Ser Asp Leu His Leu Ser Ser
 405 410 415
 Lys Ala Gln Val Phe Glu His Pro His Ile Gln Asp Ala Ala Ser Gln
 420 425 430
 Leu Pro Asp Asp Glu Ser Leu Phe Phe Gly Asp Thr Gly Leu Ser Lys
 435 440 445
 Asn Pro Ile Glu Leu Val Glu Gly Trp Phe Ser Ser Trp Lys Ser Ser
 450 455 460
 Ile Ala Ser Phe Phe Phe Ile Ile Gly Leu Ile Ile Gly Leu Phe Leu
 465 470 475 480
 Val Leu Arg Val Gly Ile His Leu Cys Ile Lys Leu Lys His Thr Lys
 485 490 495
 Lys Arg Gln Ile Tyr Thr Asp Ile Glu Met Asn Arg Leu Gly Lys

500

505

510

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2109 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```

Met Glu Val His Asp Phe Glu Thr Asp Glu Phe Asn Asp Phe Asn Glu
 1           5           10           15
Asp Asp Tyr Ala Thr Arg Glu Phe Leu Asn Pro Asp Glu Arg Met Thr
          20           25           30
Tyr Leu Asn His Ala Asp Tyr Asn Leu Asn Ser Pro Leu Ile Ser Asp
          35           40           45
Asp Ile Asp Asn Leu Ile Arg Lys Phe Asn Ser Leu Pro Ile Pro Ser
          50           55           60
Met Trp Asp Ser Lys Asn Trp Asp Gly Val Leu Glu Met Leu Thr Ser
          65           70           75           80
Cys Gln Ala Asn Pro Ile Ser Thr Ser Gln Met His Lys Trp Met Gly
          85           90           95
Ser Trp Leu Met Ser Asp Asn His Asp Ala Ser Gln Gly Tyr Ser Phe
          100          105          110
Leu His Glu Val Asp Lys Glu Ala Glu Ile Thr Phe Asp Val Val Glu
          115          120          125
Thr Phe Ile Arg Gly Trp Gly Asn Lys Pro Ile Glu Tyr Ile Lys Lys
          130          135          140
Glu Arg Trp Thr Asp Ser Phe Lys Ile Leu Ala Tyr Leu Cys Gln Lys
          145          150          155          160
Phe Leu Asp Leu His Lys Leu Thr Leu Ile Leu Asn Ala Val Ser Glu
          165          170          175
Val Glu Leu Leu Asn Leu Ala Arg Thr Phe Lys Gly Lys Val Arg Arg
          180          185          190
Ser Ser His Gly Thr Asn Ile Cys Arg Ile Arg Val Pro Ser Leu Gly
          195          200          205
Pro Thr Phe Ile Ser Glu Gly Trp Ala Tyr Phe Lys Lys Leu Asp Ile
          210          215          220
Leu Met Asp Arg Asn Phe Leu Leu Met Val Lys Asp Val Ile Ile Gly
          225          230          235          240
Arg Met Gln Thr Val Leu Ser Met Val Cys Arg Ile Asp Asn Leu Phe
          245          250          255
Ser Glu Gln Asp Ile Phe Ser Leu Leu Asn Ile Tyr Arg Ile Gly Asp
          260          265          270
Lys Ile Val Glu Arg Gln Gly Asn Phe Ser Tyr Asp Leu Ile Lys Met

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275					280					285					
Val	Glu	Pro	Ile	Cys	Asn	Leu	Lys	Leu	Met	Lys	Leu	Ala	Arg	Glu	Ser
290						295					300				
Arg	Pro	Leu	Val	Pro	Gln	Phe	Pro	His	Phe	Glu	Asn	His	Ile	Lys	Thr
305					310					315				320	
Ser	Val	Asp	Glu	Gly	Ala	Lys	Ile	Asp	Arg	Gly	Ile	Arg	Phe	Leu	His
				325					330					335	
Asp	Gln	Ile	Met	Ser	Val	Lys	Thr	Val	Asp	Leu	Thr	Leu	Val	Ile	Tyr
			340					345					350		
Gly	Ser	Phe	Arg	His	Trp	Gly	His	Pro	Phe	Ile	Asp	Tyr	Tyr	Thr	Gly
		355				360						365			
Leu	Glu	Lys	Leu	His	Ser	Gln	Val	Thr	Met	Lys	Lys	Asp	Ile	Asp	Val
	370					375					380				
Ser	Tyr	Ala	Lys	Ala	Leu	Ala	Ser	Asp	Leu	Ala	Arg	Ile	Val	Leu	Phe
385					390					395					400
Gln	Gln	Phe	Asn	Asp	His	Lys	Lys	Trp	Phe	Val	Asn	Gly	Asp	Leu	Leu
			405						410					415	
Pro	His	Asp	His	Pro	Phe	Lys	Ser	His	Val	Lys	Glu	Asn	Thr	Trp	Pro
			420					425					430		
Thr	Ala	Ala	Gln	Val	Gln	Asp	Phe	Gly	Asp	Lys	Trp	His	Glu	Leu	Pro
		435				440						445			
Leu	Ile	Lys	Cys	Phe	Glu	Ile	Pro	Asp	Leu	Leu	Asp	Pro	Ser	Ile	Ile
	450					455					460				
Tyr	Ser	Asp	Lys	Ser	His	Ser	Met	Asn	Arg	Ser	Glu	Val	Leu	Lys	His
465					470					475					480
Val	Arg	Met	Asn	Pro	Asn	Thr	Pro	Ile	Pro	Ser	Lys	Lys	Val	Leu	Gln
			485						490					495	
Thr	Met	Leu	Asp	Thr	Lys	Ala	Thr	Asn	Trp	Lys	Glu	Phe	Leu	Lys	Glu
			500					505					510		
Ile	Asp	Glu	Lys	Gly	Leu	Asp	Asp	Asp	Asp	Leu	Ile	Ile	Gly	Leu	Lys
		515				520						525			
Gly	Lys	Glu	Arg	Glu	Leu	Lys	Leu	Ala	Gly	Arg	Phe	Phe	Ser	Leu	Met
	530					535					540				
Ser	Trp	Lys	Leu	Arg	Glu	Tyr	Phe	Val	Ile	Thr	Glu	Tyr	Leu	Ile	Lys
545					550					555					560
Thr	His	Phe	Val	Pro	Met	Phe	Lys	Gly	Leu	Thr	Met	Ala	Asp	Asp	Leu
			565						570					575	
Thr	Ala	Val	Ile	Lys	Lys	Met	Leu	Asp	Ser	Ser	Ser	Gly	Gln	Gly	Leu
			580					585					590		
Lys	Ser	Tyr	Glu	Ala	Ile	Cys	Ile	Ala	Asn	His	Ile	Asp	Tyr	Glu	Lys
		595					600					605			
Trp	Asn	Asn	His	Gln	Arg	Lys	Leu	Ser	Asn	Gly	Pro	Val	Phe	Arg	Val
	610					615					620				
Met	Gly	Gln	Phe	Leu	Gly	Tyr	Pro	Ser	Leu	Ile	Glu	Arg	Thr	His	Glu
625					630					635					640

Phe Phe Glu Lys Ser Leu Ile Tyr Tyr Asn Gly Arg Pro Asp Leu Met
 645 650 655
 Arg Val His Asn Asn Thr Leu Ile Asn Ser Thr Ser Gln Arg Val Cys
 660 665 670
 Trp Gln Gly Gln Glu Gly Gly Leu Glu Gly Leu Arg Gln Lys Gly Trp
 675 680 685
 Thr Ile Leu Asn Leu Leu Val Ile Gln Arg Glu Ala Lys Ile Arg Asn
 690 695 700
 Thr Ala Val Lys Val Leu Ala Gln Gly Asp Asn Gln Val Ile Cys Thr
 705 710 715 720
 Gln Tyr Lys Thr Lys Lys Ser Arg Asn Val Val Glu Leu Gln Gly Ala
 725 730 735
 Leu Asn Gln Met Val Ser Asn Asn Glu Lys Ile Met Thr Ala Ile Lys
 740 745 750
 Ile Gly Thr Gly Lys Leu Gly Leu Leu Ile Asn Asp Asp Glu Thr Met
 755 760 765
 Gln Ser Ala Asp Tyr Leu Asn Tyr Gly Lys Ile Pro Ile Phe Arg Gly
 770 775 780
 Val Ile Arg Gly Leu Glu Thr Lys Arg Trp Ser Arg Val Thr Cys Val
 785 790 795 800
 Thr Asn Asp Gln Ile Pro Thr Cys Ala Asn Ile Met Ser Ser Val Ser
 805 810 815
 Thr Asn Ala Leu Thr Val Ala His Phe Ala Glu Asn Pro Ile Asn Ala
 820 825 830
 Met Ile Gln Tyr Asn Tyr Phe Gly Thr Phe Ala Arg Leu Leu Leu Met
 835 840 845
 Met His Asp Pro Ala Leu Arg Gln Ser Leu Tyr Glu Val Gln Asp Lys
 850 855 860
 Ile Pro Gly Leu His Ser Ser Thr Phe Lys Tyr Ala Met Leu Tyr Leu
 865 870 875 880
 Asp Pro Ser Ile Gly Gly Val Ser Gly Met Ser Leu Ser Arg Phe Leu
 885 890 895
 Ile Arg Ala Phe Pro Asp Pro Val Thr Glu Ser Leu Ser Phe Trp Arg
 900 905 910
 Phe Ile His Val His Ala Arg Ser Glu His Leu Lys Glu Met Ser Ala
 915 920 925
 Val Phe Gly Asn Pro Glu Ile Ala Lys Phe Arg Ile Thr His Ile Asp
 930 935 940
 Lys Leu Val Glu Asp Pro Thr Ser Leu Asn Ile Ala Met Gly Met Ser
 945 950 955 960
 Pro Ala Asn Leu Leu Lys Thr Glu Val Lys Lys Cys Leu Ile Glu Ser
 965 970 975
 Arg Gln Thr Ile Arg Asn Gln Val Ile Lys Asp Ala Thr Ile Tyr Leu
 980 985 990
 Tyr His Glu Glu Asp Arg Leu Arg Ser Phe Leu Trp Ser Ile Asn Pro

995					1000					1005					
Leu	Phe	Pro	Arg	Phe	Leu	Ser	Glu	Phe	Lys	Ser	Gly	Thr	Phe	Leu	Gly
1010					1015					1020					
Val	Ala	Asp	Gly	Leu	Ile	Ser	Leu	Phe	Gln	Asn	Ser	Arg	Thr	Ile	Arg
1025					1030					1035					1040
Asn	Ser	Phe	Lys	Lys	Lys	Tyr	His	Arg	Glu	Leu	Asp	Asp	Leu	Ile	Val
				1045					1050					1055	
Arg	Ser	Glu	Val	Ser	Ser	Leu	Thr	His	Leu	Gly	Lys	Leu	His	Leu	Arg
			1060					1065					1070		
Arg	Gly	Ser	Cys	Lys	Met	Trp	Thr	Cys	Ser	Ala	Thr	His	Ala	Asp	Thr
			1075				1080					1085			
Leu	Arg	Tyr	Lys	Ser	Trp	Gly	Arg	Thr	Val	Ile	Gly	Thr	Thr	Val	Pro
1090					1095					1100					
His	Pro	Leu	Glu	Met	Leu	Gly	Pro	Gln	His	Arg	Lys	Glu	Thr	Pro	Cys
1105					1110					1115					1120
Ala	Pro	Cys	Asn	Thr	Ser	Gly	Phe	Asn	Tyr	Val	Ser	Val	His	Cys	Pro
				1125					1130					1135	
Asp	Gly	Ile	His	Asp	Val	Phe	Ser	Ser	Arg	Gly	Pro	Leu	Pro	Ala	Tyr
			1140					1145					1150		
Leu	Gly	Ser	Lys	Thr	Ser	Glu	Ser	Thr	Ser	Ile	Leu	Gln	Pro	Trp	Glu
			1155				1160					1165			
Arg	Glu	Ser	Lys	Val	Pro	Leu	Ile	Lys	Arg	Ala	Thr	Arg	Leu	Arg	Asp
1170					1175					1180					
Ala	Ile	Ser	Trp	Phe	Val	Glu	Pro	Asp	Ser	Lys	Leu	Ala	Met	Thr	Ile
1185					1190					1195					1200
Leu	Ser	Asn	Ile	His	Ser	Leu	Thr	Gly	Glu	Glu	Trp	Thr	Lys	Arg	Gln
			1205						1210					1215	
His	Gly	Phe	Lys	Arg	Thr	Gly	Ser	Ala	Leu	His	Arg	Phe	Ser	Thr	Ser
			1220					1225					1230		
Arg	Met	Ser	His	Gly	Gly	Phe	Ala	Ser	Gln	Ser	Thr	Ala	Ala	Leu	Thr
			1235				1240					1245			
Arg	Leu	Met	Ala	Thr	Thr	Asp	Thr	Met	Arg	Asp	Leu	Gly	Asp	Gln	Asn
1250					1255					1260					
Phe	Asp	Phe	Leu	Phe	Gln	Ala	Thr	Leu	Leu	Tyr	Ala	Gln	Ile	Thr	Thr
1265					1270					1275					1280
Thr	Val	Ala	Arg	Asp	Gly	Trp	Ile	Thr	Ser	Cys	Thr	Asp	His	Tyr	His
			1285						1290					1295	
Ile	Ala	Cys	Lys	Ser	Cys	Leu	Arg	Pro	Ile	Glu	Glu	Ile	Thr	Leu	Asp
			1300					1305					1310		
Ser	Ser	Met	Asp	Tyr	Thr	Pro	Pro	Asp	Val	Ser	His	Val	Leu	Lys	Thr
			1315				1320					1325			
Trp	Arg	Asn	Gly	Glu	Gly	Ser	Trp	Gly	Gln	Glu	Ile	Lys	Gln	Ile	Tyr
1330					1335					1340					
Pro	Leu	Glu	Gly	Asn	Trp	Lys	Asn	Leu	Ala	Pro	Ala	Glu	Gln	Ser	Tyr
1345					1350					1355					1360

Gln Val Gly Arg Cys Ile Gly Phe Leu Tyr Gly Asp Leu Ala Tyr Arg
 1365 1370 1375
 Lys Ser Thr His Ala Glu Asp Ser Ser Leu Phe Pro Leu Ser Ile Gln
 1380 1385 1390
 Gly Arg Ile Arg Gly Arg Gly Phe Leu Lys Gly Leu Leu Asp Gly Leu
 1395 1400 1405
 Met Arg Ala Ser Cys Cys Gln Val Ile His Arg Arg Ser Leu Ala His
 1410 1415 1420
 Leu Lys Arg Pro Ala Asn Ala Val Tyr Gly Gly Leu Ile Tyr Leu Ile
 1425 1430 1435 1440
 Asp Lys Leu Ser Val Ser Pro Pro Phe Leu Ser Leu Thr Arg Ser Gly
 1445 1450 1455
 Pro Ile Arg Asp Glu Leu Glu Thr Ile Pro His Lys Ile Pro Thr Ser
 1460 1465 1470
 Tyr Pro Thr Ser Asn Arg Asp Met Gly Val Ile Val Arg Asn Tyr Phe
 1475 1480 1485
 Lys Tyr Gln Cys Arg Leu Ile Glu Lys Gly Lys Tyr Arg Ser His Tyr
 1490 1495 1500
 Ser Gln Leu Trp Leu Phe Ser Asp Val Leu Ser Ile Asp Phe Ile Gly
 1505 1510 1515 1520
 Pro Phe Ser Ile Ser Thr Thr Leu Leu Gln Ile Leu Tyr Lys Pro Phe
 1525 1530 1535
 Leu Ser Gly Lys Asp Lys Asn Glu Leu Arg Glu Leu Ala Asn Leu Ser
 1540 1545 1550
 Ser Leu Leu Arg Ser Gly Glu Gly Trp Glu Asp Ile His Val Lys Phe
 1555 1560 1565
 Phe Thr Lys Asp Ile Leu Leu Cys Pro Glu Glu Ile Arg His Ala Cys
 1570 1575 1580
 Lys Phe Gly Ile Ala Lys Asp Asn Asn Lys Asp Met Ser Tyr Pro Pro
 1585 1590 1595 1600
 Trp Gly Arg Glu Ser Arg Gly Thr Ile Thr Thr Ile Pro Val Tyr Tyr
 1605 1610 1615
 Thr Thr Thr Pro Tyr Pro Lys Met Leu Glu Met Pro Pro Arg Ile Gln
 1620 1625 1630
 Asn Pro Leu Leu Ser Gly Ile Arg Leu Gly Gln Leu Pro Thr Gly Ala
 1635 1640 1645
 His Tyr Lys Ile Arg Ser Ile Leu His Gly Met Gly Ile His Tyr Arg
 1650 1655 1660
 Asp Phe Leu Ser Cys Gly Asp Gly Ser Gly Gly Met Thr Ala Ala Leu
 1665 1670 1675 1680
 Leu Arg Glu Asn Val His Ser Arg Gly Ile Phe Asn Ser Leu Leu Glu
 1685 1690 1695
 Leu Ser Gly Ser Val Met Arg Gly Ala Ser Pro Glu Pro Pro Ser Ala
 1700 1705 1710
 Leu Glu Thr Leu Gly Gly Asp Lys Ser Arg Cys Val Asn Gly Glu Thr

1715					1720					1725					
Cys	Trp	Glu	Tyr	Pro	Ser	Asp	Leu	Cys	Asp	Pro	Arg	Thr	Trp	Asp	Tyr
1730						1735					1740				
Phe	Leu	Arg	Leu	Lys	Ala	Gly	Leu	Gly	Leu	Gln	Ile	Asp	Leu	Ile	Val
1745					1750					1755					1760
Met	Asp	Met	Glu	Val	Arg	Asp	Ser	Ser	Thr	Ser	Leu	Lys	Ile	Glu	Thr
				1765					1770					1775	
Asn	Val	Arg	Asn	Tyr	Val	His	Arg	Ile	Leu	Asp	Glu	Gln	Gly	Val	Leu
			1780					1785					1790		
Ile	Tyr	Lys	Thr	Tyr	Gly	Thr	Tyr	Ile	Cys	Glu	Ser	Glu	Lys	Asn	Ala
		1795					1800					1805			
Val	Thr	Ile	Leu	Gly	Pro	Met	Phe	Lys	Thr	Val	Asp	Leu	Val	Gln	Thr
	1810					1815					1820				
Glu	Phe	Ser	Ser	Ser	Gln	Thr	Ser	Glu	Val	Tyr	Met	Val	Cys	Lys	Gly
1825					1830					1835					1840
Leu	Lys	Lys	Leu	Ile	Asp	Glu	Pro	Asn	Pro	Asp	Trp	Ser	Ser	Ile	Asn
				1845					1850					1855	
Glu	Ser	Trp	Lys	Asn	Leu	Tyr	Ala	Phe	Gln	Ser	Ser	Glu	Gln	Glu	Phe
			1860					1865					1870		
Ala	Arg	Ala	Lys	Lys	Val	Ser	Thr	Tyr	Phe	Thr	Leu	Thr	Gly	Ile	Pro
			1875				1880						1885		
Ser	Gln	Phe	Ile	Pro	Asp	Pro	Phe	Val	Asn	Ile	Glu	Thr	Met	Leu	Gln
	1890					1895					1900				
Ile	Phe	Gly	Val	Pro	Thr	Gly	Val	Ser	His	Ala	Ala	Ala	Leu	Lys	Ser
1905					1910					1915					1920
Ser	Asp	Arg	Pro	Ala	Asp	Leu	Leu	Thr	Ile	Ser	Leu	Phe	Tyr	Met	Ala
				1925					1930					1935	
Ile	Ile	Ser	Tyr	Tyr	Asn	Ile	Asn	His	Ile	Arg	Val	Gly	Pro	Ile	Pro
			1940					1945					1950		
Pro	Asn	Pro	Pro	Ser	Asp	Gly	Ile	Ala	Gln	Asn	Val	Gly	Ile	Ala	Ile
	1955					1960						1965			
Thr	Gly	Ile	Ser	Phe	Trp	Leu	Ser	Leu	Met	Glu	Lys	Asp	Ile	Pro	Leu
	1970					1975					1980				
Tyr	Gln	Gln	Cys	Leu	Ala	Val	Ile	Gln	Gln	Ser	Phe	Pro	Ile	Arg	Trp
1985					1990					1995					2000
Glu	Ala	Val	Ser	Val	Lys	Gly	Gly	Tyr	Lys	Gln	Lys	Trp	Ser	Thr	Arg
				2005					2010					2015	
Gly	Asp	Gly	Leu	Pro	Lys	Asp	Thr	Arg	Thr	Ser	Asp	Ser	Leu	Ala	Pro
			2020					2025					2030		
Ile	Gly	Asn	Trp	Ile	Arg	Ser	Leu	Glu	Leu	Val	Arg	Asn	Gln	Val	Arg
		2035					2040						2045		
Leu	Asn	Pro	Phe	Asn	Glu	Ile	Leu	Phe	Asn	Gln	Leu	Cys	Arg	Thr	Val
	2050					2055					2060				
Asp	Asn	His	Leu	Lys	Trp	Ser	Asn	Leu	Arg	Arg	Asn	Thr	Gly	Met	Ile
2065					2070					2075					2080

Glu Trp Ile Asn Arg Arg Ile Ser Lys Glu Asp Arg Ser Ile Leu Met
 2085 2090 2095

Leu Lys Ser Asp Leu His Glu Glu Asn Ser Trp Arg Asp
 2100 2105

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 14311 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

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AGAGTATGAG TATTCAACAT TTCCGTGTCTG CCCTTATTCC CTTTTTTCG GCATTTTGCC	180
TTCTGTGTTT TGCTCACCCA GAAACGCTGG TGAAAGTAAA AGATGCTGAA GATCAGTTGG	240
GTGCACGAGT GGGTTACATC GAACTGGATC TCAACAGCGG TAAGATCCTT GAGAGTTTTT	300
GCCCCGAAGA ACGTTTTCCT ATGATGAGCA CTTTAAAGT TCTGCTATGT GGCGCGGTAT	360
TATCCCGTAT TGACGCCGGG CAAGAGCAAC TCGGTGCGG CATACTAT CTCAGAATG	420
ACTTGGTTGA GTACTACCA GTCACAGAAA AGCATCTTAC GGATGGCATG ACAGTAAGAG	480
AATTATGCAG TGCTGCCATA ACCATGAGTG ATAACACTGC GGCCAACCTA CTTCTGACAA	540
CGATCGGAGG ACCGAAGGAG CTAACCGCTT TTTTGCACAA CATGGGGGAT CATGTAAGTC	600
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TGCGCTCGGC CCTTCCGGCT GGCTGGTTTA TTGCTGATAA ATCTGGAGCC GGTGAGCGTG	840
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 GATACAAAGG CAACCATTG TCATCTGCGC TGGTCTGGA AGCATCCGAT ACTCCATCTG 13200
 GAAGTACGCC GTCCAGGGCT TTCAAGGATA CAAGGTCAAA TATTCCGATT GTATCCCCTG 13260
 CTTTCCCGAT GTTTATTCCG AAACCTGACC AATCTTTATC CAACTTACCC CGGATGTCCT 13320
 TTAATGCTCC ATACAAGTAG CTGTTGACAT GTATGATTGA TACATTTCCG GATTTGAGGC 13380
 CTTGGTAGAC ATATCCTCTT AGATCTGACA AACTTTTTGT AGTATTGATG TAAAGAGGAA 13440
 TCTCCTTTGA TTTTCTGAAG TAATCTGCCG GGTATTCCAC TGGATCCTCA TTTGCAGGAA 13500
 GTTTTGGAAC TATGACTGTG TTGTCAATGA TTCTCTTGAC TGTAACAGAC ATTTTGATTA 13560
 CTGTTAAAGT TTCTCCTGAG CCTTTTAATG ATAATAATGG TTTGTTTGTC TTCGTCCCTA 13620

TAGTGAGTCG TATTACAACT CGAGGGGGGG CCCGGTACCC AATTCGCCCT ATAGTGAGTC 13680
 GTATTACAAT TCACTGGCCG TCGTTTTACA ACGTCGTGAC TGGGAAAACC CTGGCGTTAC 13740
 CCAACTTAAT CGCCTTGCAG CACATCCCCC TTTCGCCAGC TGGCGTAATA GCGAAGAGGC 13800
 CCGCACCGAT CGCCCTTCCC AACAGTTGCG CAGCCTGAAT GGCGAATGGG ACGCGCCCTG 13860
 TAGCGGCGCA TTAAGCGCGG CGGGTGTGGT GGTACGCGC AGCGTGACCG CTACACTTGC 13920
 CAGCGCCCTA GCGCCCGCTC CTTTCGCTTT CTCCCTTCC TTTCTCGCCA CGTTCGCCGG 13980
 CTTTCCCCGT CAAGCTCTAA ATCGGGGGCT CCCTTTAGGG TTCCGATTTA GTGCTTTACG 14040
 GCACCTCGAC CCCAAAAAAC TTGATTAGGG TGATGGTTCA CGTAGTGGGC CATCGCCCTG 14100
 ATAGACGGTT TTTCGCCCTT TGACGTTGGA GTCCACGTTT TTTAATAGTG GACTCTTGTT 14160
 CCAAACTGGA ACAAACTCA ACCCTATCTC GGTCTATTCT TTTGATTTAT AAGGGATTTT 14220
 GCCGATTTTC GCCTATTGGT TAAAAAATGA GCTGATTAA CAAAAATTTA ACGCGAATTT 14280
 TAACAAAATA TTAACGCTTA CAATTTAGGT G 14311

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TTGTAATACG ACTCACTATA GGG

23

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTGTAATACG ACTCACTATA GGG

23

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ACGAAGACAA ACAACCATT ATTATCATTA AAAGGCTCAG GAGAACTTT

50

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGCTGCTAAC AAAGCCCGAA AGGAAGCTGA GTTGGCTGCT GCCACCGCTG AGCAATAACT

60

AGCATAACCC CTTGGGGCCT CTAAACGGGT CTTGAGGGGT TTTTGTCTGA AAGGAGGAAC

120

TATATCCGGA TCGAGA

136

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGGTCGGCAT GGCATCTCCA CCTCCTCGCG GTCCGACCTG GGCATCCGAA GGAGGACGTC

60

GTCCACTCGG ATGGCTAAGG GAG

83

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 630 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TTGTAGAAGG TTGGTTCAGT AGTTGGAAAA GCTCTATTGC CTCTTTTTTC TTTATCATAG

60

GGTTAATCAT TGGACTATTC TTGGTTCTCC GAGTTGGTAT CCATCTTTGC ATTAAATTAA

120

AGCACACCAA GAAAAGACAG ATTTATACAG ACATAGAGAT GAACCGACTT GGAAAGTAAC

180

TCAAATCCTG CTAGCTATGA AAAAACTAA CAGATATCCA ACCCGGGAGC TAGTTGCGGC 240
 CGCCTAGCAG ATTCTTCATG TTTGGACCAA ATCAACTTGT GATACCATGC TCAAAGAGGC 300
 CTCAATTATA TTTGAGTTTT TAATTTTTAT GAAAAAACT AACAGCAATC ATGGAAGTCC 360
 ACGATTTTGA GACCGACGAG TTCAATGATT TCAATGAAGA TGACTATGCC ACAAGAGAAT 420
 TCCTGAATCC CGATGAGCGC ATGACGTACT TGAATCATGC TGATTACAAT TTGAATTCTC 480
 CTCTAATTAG TGATGATATT GACAATTTGA TCAGGAAATT CAATTCTCTT CCGATTCCCT 540
 CGATGTGGGA TAGTAAGAAC TGGGATGGAG TTCTTGAGAT GTTAACATCA TGTCAGCCA 600
 ATCCCATCTC AACATCTCAG ATGCATAAAT 630

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 630 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATTTATGCAT CTGAGATGTT GAGATGGGAT TGGCTTGACA TGATGTTAAC ATCTCAAGAA 60
 CTCCATCCCA GTTCTTACTA TCCACATCG AGGGAAAGG AAGAGATTG AATTCCTGA 120
 TCAAATTGTC AATATCATCA CTAATTAGAG GAGAATTCAA ATTGTAATCA GCATGATTCA 180
 AGTACGTCAT GCGCTCATCG GGATTCAGGA ATTCTCTTGT GGCATAGTCA TCTTCATTGA 240
 AATCATTGAA CTCGTCGGTC TCAAATCGT GGAATTCCAT GATTGCTGTT AGTTTTTTTC 300
 ATAAAAATTA AAAACTCAAA TATAATTGAG GCCTCTTTGA GCATGGTATC ACAAGTTGAT 360
 TTGGTCCAAA CATGAAGAAT CTGCTAGGCG GCCGCAACTA GCTCCCGGGT TGGATATCTG 420
 TTAGTTTTTT TCATAGCTAG CAGGATTTGA GTTACTTTCC AAGTCGGTTC ATCTCTATGT 480
 CTGTATAAAT CTGTCTTTTC TTGGTGTGCT TTAATTTAAT GCAAAGATGG ATACCAACTC 540
 GGAGAACCAA GAATAGTCCA ATGATTAACC CTATGATAAA GAAAAAGAG GCAATAGAGC 600
 TTTTCCAAC ACTGAACCAA CCTTCTACAA 630

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: RNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

UCAGGAGAAA C

11

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: RNA

(ix) FEATURE:

- (A) NAME/KEY: 5' Gppp
- (B) LOCATION: 1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AACAGUAAUC

10

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: RNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GAUUACUGUU AAAGUUUCUC CUGA

24

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: RNA

(ix) FEATURE:

- (A) NAME/KEY: polyA
- (B) LOCATION: 10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GCUACAU AUG

10

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: RNA

- (ix) FEATURE:
 (A) NAME/KEY: 5' Gppp
 (B) LOCATION: 1

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AACAGAUUUC

10

- (2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: RNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GAUAUCUGUU AGUUUUUUUC AUAUGUAGC

29

- (2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: RNA

- (ix) FEATURE:
 (A) NAME/KEY: polyA
 (B) LOCATION: 10

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GUAGACUAUG

10

- (2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: RNA

- (ix) FEATURE:
 (A) NAME/KEY: 5' Gppp
 (B) LOCATION: 1

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AACAGAUUUC

10

- (2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: RNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GAUAUCUGUU ACUUUUUUUC AUAGUCUAC

29

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: RNA

(ix) FEATURE:

- (A) NAME/KEY: polyA
- (B) LOCATION: 10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

UAUCCCUAUG

10

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: RNA

(ix) FEATURE:

- (A) NAME/KEY: 5' Gppp
- (B) LOCATION: 1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AACAGAGAU

10

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: RNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GAUCUCUGUU AGUUUUUUUC AUAGGGAUA

29

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA

(ix) FEATURE:

- (A) NAME/KEY: polyA
 (B) LOCATION: 10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

AAUUUUUAUG

10

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA

(ix) FEATURE:

- (A) NAME/KEY: 5' Gppp
 (B) LOCATION: 1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AACAGCAAUC

10

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: RNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GAUUGCUGUU AGUUUUUUUC AUAAAAAUU

29

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: RNA

(ix) FEATURE:

(A) NAME/KEY: polyA

(B) LOCATION: 10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

UUUAAGUAUG

10

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: RNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

AGGAUCAAAG UUUUUUCAU ACUAAA

27

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CATTCAAGAC GCTGCTTCGC AACTTCC

27

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CATGAATGTT AACATCTCAA GA

22

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA

- (ix) FEATURE:
 - (A) NAME/KEY: miscellaneous feature
 - (B) LOCATION: 11..12
 - (D) OTHER INFORMATION: Intergenic dinucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GAUNNCUGUU ANUUUUUUUC AUA

23

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: RNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

UAUGAAAAAA A

11

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: RNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

UUUUUUUCAU A

11

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

TATGAAAAAA A

11

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CCGGCTCGAG TTGTAATACG ACTCACTATA GGGACGAAGA CAAACAAACC ATTATTATC

59

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GAACTCTCCT CTAGATGAGA AC

22

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 58 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

AGGTCGGACC GCGAGGAGGT GGAGATGCCA TGCCGACCCA CGAAGACCAC AAAACCAG

58

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

WO 96/34625

PCT/US96/06053

ATGTTGAAGA GTGACCTACA CG

22

WHAT IS CLAIMED IS:

1. A recombinant replicable vesiculovirus, the genome of which comprises a foreign RNA sequence.
5
2. The vesiculovirus of claim 1 in which an RNA sequence complementary to said foreign RNA sequence encodes a peptide or protein that is expressed in a suitable host infected by the virus.
10
3. The vesiculovirus of claim 1 in which the peptide or protein is antigenic or immunogenic.
4. The vesiculovirus of claim 2 in which the
15 peptide or protein displays the antigenicity or immunogenicity of an antigen of a pathogenic microorganism.
5. The vesiculovirus of claim 4 in which the pathogenic microorganism is a virus.
20
6. The vesiculovirus of claim 4 in which the pathogenic microorganism is a bacterium.
7. The vesiculovirus of claim 4 in which the
25 pathogenic microorganism is a parasite.
8. The vesiculovirus of claim 4 in which the pathogenic microorganism is a human pathogen..
- 30 9. The vesiculovirus of claim 4 in which the pathogenic microorganism is a non-human pathogen.
10. The vesiculovirus of claim 2 in which the peptide or protein displays the antigenicity or
35 immunogenicity of a tumor specific or tumor associated antigen.

11. Plasmid pVSVFL(+), as deposited with the ATCC and assigned accession number 97134.

12. A nucleic acid comprising the DNA sequence of 5 plasmid pVSVFL(+) as depicted in Figure 1 from nucleotide numbers 623-12088 (a portion of SEQ ID NO:1), in which a region nonessential for vesiculovirus replication has been inserted into or replaced by foreign DNA.

10 13. A host cell containing the recombinant vesiculovirus of claim 1.

14. A method of producing a recombinant vesiculovirus comprising culturing a cell containing (a) a 15 recombinant nucleic acid that can be transcribed to produce an RNA molecule comprising a vesiculovirus antigenomic (+) RNA, in which a region of the RNA nonessential for replication of the vesiculovirus has been inserted into or replaced by a foreign RNA sequence; (b) a second recombinant 20 nucleic acid encoding a vesiculovirus N protein; (c) a third recombinant nucleic acid encoding a vesiculovirus L protein; and (d) a fourth recombinant nucleic acid encoding a vesiculovirus P protein; whereby the first recombinant nucleic acid is transcribed in the cell to produce said RNA 25 molecule, and the N, L and P proteins are expressed in the cell, and a recombinant replicable vesiculovirus is produced that has a genome that is the complement of said antigenomic RNA comprising said foreign RNA sequence.

30 15. The method according to claim 14 in which the cell is a mammalian cell.

16. The method according to claim 14 in which the first recombinant nucleic acid comprises a first promoter 35 sequence which controls the expression of the RNA molecule in the cell; the second recombinant nucleic acid comprises a second promoter sequence which controls the expression of the

N protein in the cell; the third recombinant nucleic acid comprises a third promoter sequence which controls the expression of the P protein in the cell; and the fourth recombinant nucleic acid comprises a fourth promoter sequence
5 which controls the expression of the L protein in the cell.

17. The method according to claim 14 in which said RNA molecule further comprises a ribozyme sequence immediately downstream of said antigenomic (+) RNA, that
10 cleaves at the 3' terminus of the antigenomic (+) RNA.

18. The method according to claim 14 in which the first recombinant nucleic acid is a DNA plasmid vector comprising the following operatively linked components:

- 15 (a) a promoter;
(b) a DNA sequence that can be transcribed under the control of the promoter in the cell to produce said RNA molecule; and
(c) a transcription termination signal.

20

19. The method according to claim 14 or 18 in which the second recombinant nucleic acid is a DNA plasmid vector comprising the following operatively linked components:

- 25 (a) a promoter which controls the expression of the N protein;
(b) a translation initiation signal;
(c) a DNA sequence encoding the N protein; and
30 (d) a transcription termination signal; and

in which the third recombinant nucleic acid is a DNA plasmid vector comprising the following operatively linked components:

- 35 (a) a promoter which controls the expression of the P protein;
(b) a translation initiation signal;

(c) a DNA sequence encoding the P protein;
and
(d) a transcription termination signal; and
and in which the fourth recombinant nucleic acid is a DNA
5 plasmid vector comprising the following operatively linked
components:

- 10 (a) a promoter which controls the expression
of the L protein;
(b) a translation initiation signal;
(c) a DNA sequence encoding the L protein;
and
(d) a transcription termination signal.

20. The method according to claim 17 in which the
15 first recombinant nucleic acid is a DNA plasmid vector
comprising the following operatively linked components:

- (a) a promoter;
(b) a DNA sequence that can be transcribed
under the control of the promoter in the
20 cell to produce said RNA molecule; and
(c) a transcription termination signal.

21. The method according to claim 19 in which the
first recombinant nucleic acid, the second recombinant
25 nucleic acid, the third recombinant nucleic acid, and the
fourth recombinant nucleic acid, each further comprises a
selectable marker.

22. The method according to claim 14 in which the
30 second, third and fourth recombinant nucleic acids form part
of a single recombinant nucleic acid.

23. The method according to claim 16 in which the
first, second, third and fourth promoter sequences are RNA
35 polymerase promoter sequences for the same RNA polymerase,
and in which the cell also contains a cytoplasmic source of
said RNA polymerase.

24. The method according to claim 23 in which the cytoplasmic source of said RNA polymerase is a recombinant vaccinia virus expressing said RNA polymerase in the cell.

5 25. A method of producing a recombinant vesiculovirus comprising culturing a mammalian cell containing:

(a) a first DNA plasmid vector comprising the following operatively linked components:

- 10 (i) a bacteriophage RNA polymerase promoter;
(ii) a first DNA sequence that is transcribed in the cell to produce an RNA molecule comprising (A) a vesiculovirus antigenomic (+) RNA in which a region of
15 the RNA nonessential for replication of the vesiculovirus has been inserted into or replaced by a foreign RNA sequence, and (B) a ribozyme sequence immediately downstream of said antigenomic (+) RNA,
20 that cleaves at the 3' terminus of the antigenomic RNA; and
(iii) a transcription termination signal for the RNA polymerase;

(b) a second DNA plasmid vector comprising the
25 following operatively linked components:

- (i) the bacteriophage RNA polymerase promoter;
(ii) a second DNA sequence encoding an N protein of the vesiculovirus; and
30 (iii) a second transcription termination signal for the RNA polymerase;

(c) a third DNA plasmid vector comprising the following operatively linked components:

- 35 (i) the bacteriophage RNA polymerase promoter;
(ii) a third DNA sequence encoding a P protein of the vesiculovirus; and

- (iii) a third transcription termination signal for the RNA polymerase;
- (d) a fourth DNA plasmid vector comprising the following operatively linked components:
- 5 (i) the bacteriophage RNA polymerase promoter;
- (ii) a fourth DNA sequence encoding an L protein of the vesiculovirus; and
- (iii) a fourth transcription termination signal
- 10 for the RNA polymerase; and
- (e) a recombinant vaccinia virus comprising a sequence encoding the bacteriophage RNA polymerase; whereby in said cell the first DNA sequence is transcribed to produce said RNA molecule, the N, P, and L proteins and the
- 15 bacteriophage RNA polymerase are expressed, and a recombinant replicable vesiculovirus is produced that has a genome that is the complement of said antigenomic RNA comprising said foreign RNA sequence.

20 26. The method according to claim 25 in which the ribozyme sequence is the sequence of the hepatitis delta virus ribozyme, and the bacteriophage RNA polymerase is the T7 RNA polymerase.

25 27. The method according to claim 14 in which the foreign RNA sequence is the complement of a sequence encoding a protein or peptide that is immunogenic or antigenic.

28. The method according to claim 25 in which the

30 foreign RNA sequence is the complement of a sequence encoding a protein or peptide that is immunogenic or antigenic.

29. The method according to claim 27 or 28 in which the protein or peptide displays the antigenicity or

35 immunogenicity of an antigen of a pathogenic microorganism.

30. The method according to claim 27 or 28 in which the protein or peptide displays the antigenicity or immunogenicity of a tumor specific antigen.

5 31. The method according to claim 25 which further comprises before step (a) the step of introducing said first, second, third and fourth plasmid vectors and said recombinant vaccinia virus into said cell.

10 32. A host cell comprising (a) a recombinant nucleic acid that can be transcribed to produce an RNA molecule comprising a vesiculovirus antigenomic (+) RNA, in which a region of the RNA nonessential for replication of the vesiculovirus has been inserted into or replaced by a foreign
15 RNA sequence; (b) a second recombinant nucleic acid encoding a vesiculovirus N protein; (c) a third recombinant nucleic acid encoding a vesiculovirus L protein; and (d) a fourth recombinant nucleic acid encoding a vesiculovirus P protein.

20 33. A host cell comprising:
(a) a first DNA plasmid vector comprising the following operatively linked components:
(i) a bacteriophage RNA polymerase promoter;
(ii) a first DNA sequence that is transcribed
25 in the cell to produce an RNA molecule comprising (A) a vesiculovirus antigenomic (+) RNA in which a region of the RNA nonessential for replication of the vesiculovirus has been inserted into
30 or replaced by a foreign RNA sequence, and (B) a ribozyme sequence immediately downstream of said antigenomic (+) RNA, that cleaves at the 3' terminus of the antigenomic RNA; and
35 (iii) a transcription termination signal for the RNA polymerase;

- (b) a second DNA plasmid vector comprising the following operatively linked components:
- (i) the bacteriophage RNA polymerase promoter;
 - 5 (ii) a second DNA sequence encoding an N protein of the vesiculovirus; and
 - (iii) a second transcription termination signal for the RNA polymerase;
- (c) a third DNA plasmid vector comprising the 10 following operatively linked components:
- (i) the bacteriophage RNA polymerase promoter;
 - (ii) a third DNA sequence encoding a P protein of the vesiculovirus; and
 - 15 (iii) a third transcription termination signal for the RNA polymerase;
- (d) a fourth DNA plasmid vector comprising the following operatively linked components:
- 20 (i) the bacteriophage RNA polymerase promoter;
 - (ii) a fourth DNA sequence encoding an L protein of the vesiculovirus; and
 - (iii) a fourth transcription termination signal for the RNA polymerase; and
- 25 (e) a recombinant vaccinia virus comprising a sequence encoding the bacteriophage RNA polymerase; whereby in said cell the first DNA sequence is transcribed to produce said RNA molecule, the N, P, and L proteins and the bacteriophage RNA polymerase are expressed, and a recombinant 30 replicable vesiculovirus is produced that has a genome that is the complement of said antigenomic RNA comprising said foreign RNA sequence.

34. A vaccine formulation comprising an effective 35 immunizing amount of the vesiculovirus of claim 3; and a pharmaceutically acceptable carrier.

35. A vaccine formulation comprising an effective immunizing amount of the recombinant vesiculovirus of claim 4; and a pharmaceutically acceptable carrier.

5 36. A vaccine formulation comprising an effective immunizing amount of the recombinant vesiculovirus of claim 10; and a pharmaceutically acceptable carrier.

37. A vaccine formulation comprising an effective
10 immunizing amount of a first recombinant vesiculovirus of claim 3; an effective immunizing amount of a second recombinant vesiculovirus of claim 3; and a pharmaceutically acceptable carrier; in which said peptide or protein expressed by the first and second recombinant vesiculoviruses
15 are different.

38. The vaccine formulation of claim 37 in which the peptide or protein expressed by the first recombinant vesiculovirus displays the antigenicity or immunogenicity of
20 an antigen of a first pathogenic microorganism, and the peptide or protein expressed by the second recombinant vesiculovirus displays the antigenicity or immunogenicity of an antigen of a second, different pathogenic microorganism.

25 39. A method of treating or preventing a disease or disorder in a subject comprising administering to the subject an effective immunizing amount of the recombinant vesiculovirus of claim 3.

30 40. A method of treating or preventing a disease or disorder in a subject caused by infection by a pathogenic microorganism comprising administering to the subject an effective immunizing amount of the recombinant vesiculovirus of claim 4.

35 41. A method of treating or preventing a subject having a tumor comprising administering to the subject an

effective immunizing amount of the recombinant vesiculovirus of claim 10.

42. The method according to claim 39 in which the
5 subject is a human.

43. The method according to claim 39 in which the
subject is a non-human animal.

10 44. A kit comprising in one or more containers (a)
a first recombinant nucleic acid that can be transcribed in a
host cell to produce an RNA molecule comprising a
vesiculovirus antigenomic (+) RNA, in which a region of the
RNA nonessential for replication of the vesiculovirus has
15 been inserted into or replaced by a foreign RNA sequence; (b)
a second recombinant nucleic acid encoding and capable of
expressing in the host cell a vesiculovirus N protein; (c) a
third recombinant nucleic acid encoding and capable of
expressing in the host cell a vesiculovirus L protein; and
20 (d) a fourth recombinant nucleic acid encoding and capable of
expressing in the host cell a vesiculovirus P protein.

45. A kit comprising in one or more containers (a)
a first recombinant nucleic acid that can be transcribed in a
25 host cell to produce an RNA molecule comprising a
vesiculovirus antigenomic (+) RNA; (b) a second recombinant
nucleic acid encoding and capable of expressing in the host
cell a vesiculovirus N protein; (c) a third recombinant
nucleic acid encoding and capable of expressing in the host
30 cell a vesiculovirus L protein; and (d) a fourth recombinant
nucleic acid encoding and capable of expressing in the host
cell a vesiculovirus P protein.

46. A kit comprising in one or more containers (a)
35 a recombinant nucleic acid that can be transcribed to produce
an RNA molecule comprising a vesiculovirus antigenomic (+)

RNA; and (b) a host cell that recombinantly expresses vesiculovirus N, P, and L proteins.

47. The kit of claim 45 in which said first
5 recombinant nucleic acid further comprises a polylinker in a region that is transcribed to produce said RNA molecule, said region being nonessential for replication of the vesiculovirus.

10 48. The kit according to claim 45 in which the second recombinant nucleic acid is a DNA plasmid vector comprising the following operatively linked components:

(a) a promoter which controls the expression of the N protein;

15 (b) a translation initiation signal;

(c) a DNA sequence encoding the N protein;
and

(d) a transcription termination signal; and

in which the third recombinant nucleic acid is a DNA plasmid
20 vector comprising the following operatively linked components:

(a) a promoter which controls the expression of the P protein;

25 (b) a translation initiation signal;

(c) a DNA sequence encoding the P protein;
and

(d) a transcription termination signal

and in which the fourth recombinant nucleic acid is a DNA
plasmid vector comprising the following operatively linked
30 components:

(a) a promoter which controls the expression of the L protein;

(b) a translation initiation signal;

35 (c) a DNA sequence encoding the L protein;
and

(d) a transcription termination signal; and

in which the first recombinant nucleic acid is a DNA plasmid vector comprising the following operatively linked components:

- 5 (a) a promoter;
- (b) a DNA sequence that can be transcribed under the control of the promoter in the cell to produce said RNA molecule, said RNA molecule further comprising a
10 ribozyme sequence immediately downstream of said antigenomic (+) RNA, that cleaves at the 3' terminus of the antigenomic (+) RNA, said DNA comprising a polylinker in a region that is transcribed to produce said RNA molecule, said region being
15 nonessential for replication of the vesiculovirus; and
- (c) a transcription termination signal.

49. The kit of claim 46 in which the promoter is
20 an RNA polymerase promoter, and in which the cell also contains a cytoplasmic source of said RNA polymerase.

50. A kit comprising

- (a) in a first container a first DNA plasmid
25 vector comprising the following operatively linked components:
 - (i) a bacteriophage RNA polymerase promoter;
 - (ii) a first DNA sequence that can be
30 transcribed in a cell to produce an RNA molecule comprising (A) a vesiculovirus antigenomic (+) RNA in which a region of the RNA nonessential for replication of the vesiculovirus has been inserted into or replaced by a foreign RNA sequence,
35 and (B) a ribozyme sequence immediately downstream of said antigenomic (+) RNA,

- that cleaves at the 3' terminus of the antigenomic RNA; and
- (iii) a transcription termination signal for the RNA polymerase;
- 5 (b) in a second container a second DNA plasmid vector comprising the following operatively linked components:
- (i) the bacteriophage RNA polymerase promoter;
- 10 (ii) a second DNA sequence encoding an N protein of the vesiculovirus; and
- (iii) a second transcription termination signal for the RNA polymerase;
- (c) in a third container a third DNA plasmid
- 15 vector comprising the following operatively linked components:
- (i) the bacteriophage RNA polymerase promoter;
- (ii) a third DNA sequence encoding a P protein
- 20 of the vesiculovirus; and
- (iii) a third transcription termination signal for the RNA polymerase;
- (d) in a fourth container a fourth DNA plasmid
- vector comprising the following operatively linked
- 25 components:
- (i) the bacteriophage RNA polymerase promoter;
- (ii) a fourth DNA sequence encoding an L
- 30 protein of the vesiculovirus; and
- (iii) a fourth transcription termination signal for the RNA polymerase; and
- (e) in a fifth container a recombinant vaccinia virus comprising a sequence encoding the bacteriophage RNA polymerase.
- 35
51. A kit comprising in a container an effective immunizing amount of the vesiculovirus of claim 3.

52. The vesiculovirus of claim 1 which is a vesicular stomatitis virus.

53. The vesiculovirus of claim 4 in which the peptide or protein displays the antigenicity or immunogenicity of an envelope glycoprotein of a virus other than a vesiculovirus.

54. The vesiculovirus of claim 53 in which the envelope glycoprotein is an envelope glycoprotein of a Human Immunodeficiency Virus.

55. The vesiculovirus of claim 53 in which the peptide or protein is incorporated into the vesiculovirus envelope.

56. The vesiculovirus of claim 53 in which the peptide or protein is expressed as a fusion protein comprising the cytoplasmic domain of a vesiculovirus G protein.

57. The vesiculovirus of claim 56 in which the native G protein of the vesiculovirus is not expressed.

58. The vesiculovirus of claim 56 in which the native G protein of the vesiculovirus is also expressed.

59. The vesiculovirus of claim 3 in which a second RNA sequence complementary to said foreign RNA sequence encodes a second peptide or protein that is expressed in the suitable host, in which the first peptide or protein and the second peptide or protein display different antigenicity or immunogenicity.

60. An inactivated recombinant vesiculovirus that is the product of a method comprising inactivating a recombinant replicable vesiculovirus, the genome of which

comprises a foreign RNA sequence, in which an RNA sequence complementary to said foreign RNA sequence encodes a peptide or protein that is expressed in a suitable host infected by the recombinant replicable vesiculovirus, and in which the
5 peptide or protein is antigenic or immunogenic.

61. The vesiculovirus of claim 60 in which the peptide or protein displays the antigenicity or immunogenicity of an antigen of a pathogenic microorganism.
10

62. The vesiculovirus of claim 60 in which the peptide or protein displays the antigenicity or immunogenicity of a tumor specific or tumor associated antigen.
15

63. The vesiculovirus of claim 60 in which a second RNA sequence complementary to said foreign RNA sequence encodes a second peptide or protein that is expressed in the suitable host, in which the first peptide or
20 protein and the second peptide or protein display different antigenicity or immunogenicity.

64. The vesiculovirus of claim 60 in which the peptide or protein displays the antigenicity or
25 immunogenicity of an envelope glycoprotein of a virus other than a vesiculovirus.

65. The vesiculovirus of claim 64 in which the envelope glycoprotein is an envelope glycoprotein of a Human
30 Immunodeficiency Virus.

66. The vesiculovirus of claim 64 in which the peptide or protein is incorporated into the vesiculovirus envelope.
35

67. The vesiculovirus of claim 64 in which the peptide or protein is expressed as a fusion protein

comprising the cytoplasmic domain of a vesiculovirus G protein.

68. A vaccine formulation comprising an effective
5 immunizing amount of the vesiculovirus of claim 60; and a
pharmaceutically acceptable carrier.

69. A vaccine formulation comprising an effective
immunizing amount of the vesiculovirus of claim 64; and a
10 pharmaceutically acceptable carrier.

70. A vaccine formulation comprising an effective
immunizing amount of the vesiculovirus of claim 66; and a
pharmaceutically acceptable carrier.

15

71. A method of treating or preventing a disease
or disorder in a subject comprising administering to the
subject an effective immunizing amount of the inactivated
recombinant vesiculovirus of claim 60.

20

72. A kit comprising in a container an effective
immunizing amount of the inactivated recombinant
vesiculovirus of claim 60.

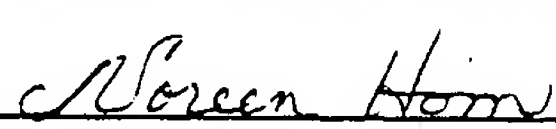
25

73. A method for producing a peptide or protein
comprising culturing a cell containing the recombinant
replicable vesiculovirus of claim 2 in said suitable host;
and recovering the expressed peptide or protein.

30

74. A method for producing an inactivated virus
vaccine comprising inactivating a recombinant replicable
vesiculovirus, the genome of which comprises a foreign RNA
sequence, in which an RNA sequence complementary to said
foreign RNA sequence encodes a peptide or protein that is
35 expressed in a suitable host infected by the recombinant
replicable vesiculovirus, and in which the peptide or protein
is antigenic or immunogenic.

International Application No: PCT/

MICROORGANISMS	
Optional Sheet in connection with the microorganism referred to on page 71, lines 15-35 of the description	
A. IDENTIFICATION OF DEPOSIT	
Further deposits are identified on an additional sheet	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, MD 20852 US	
Date of deposit: May 2, 1995 Accession Number: 97134	
B. ADDITIONAL INDICATIONS (leave blank if not applicable). This information is continued on a separate attached sheet	
C. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not all designated States)	
D. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (Specify the general nature of the indications e.g., "Accession Number of Deposit")	
E. <input checked="" type="checkbox"/> This sheet was received with the International application when filed (to be checked by the receiving Office)	
<div style="text-align: right;"> (Authorized Officer)</div>	
<input type="checkbox"/> The date of receipt (from the applicant) by the International Bureau "	
was	
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Form PCT/RO/134 (January 1981)

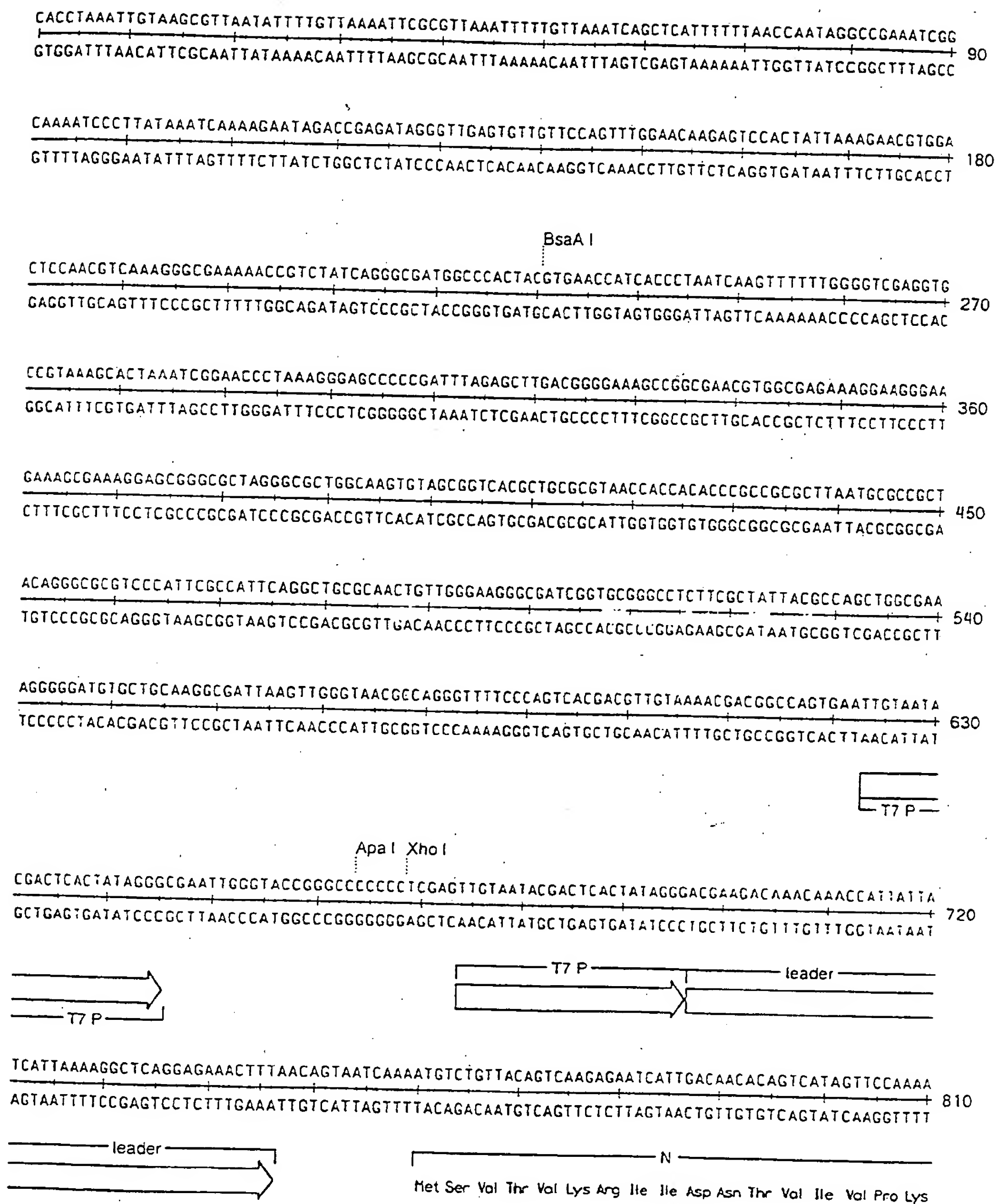


FIG. 1

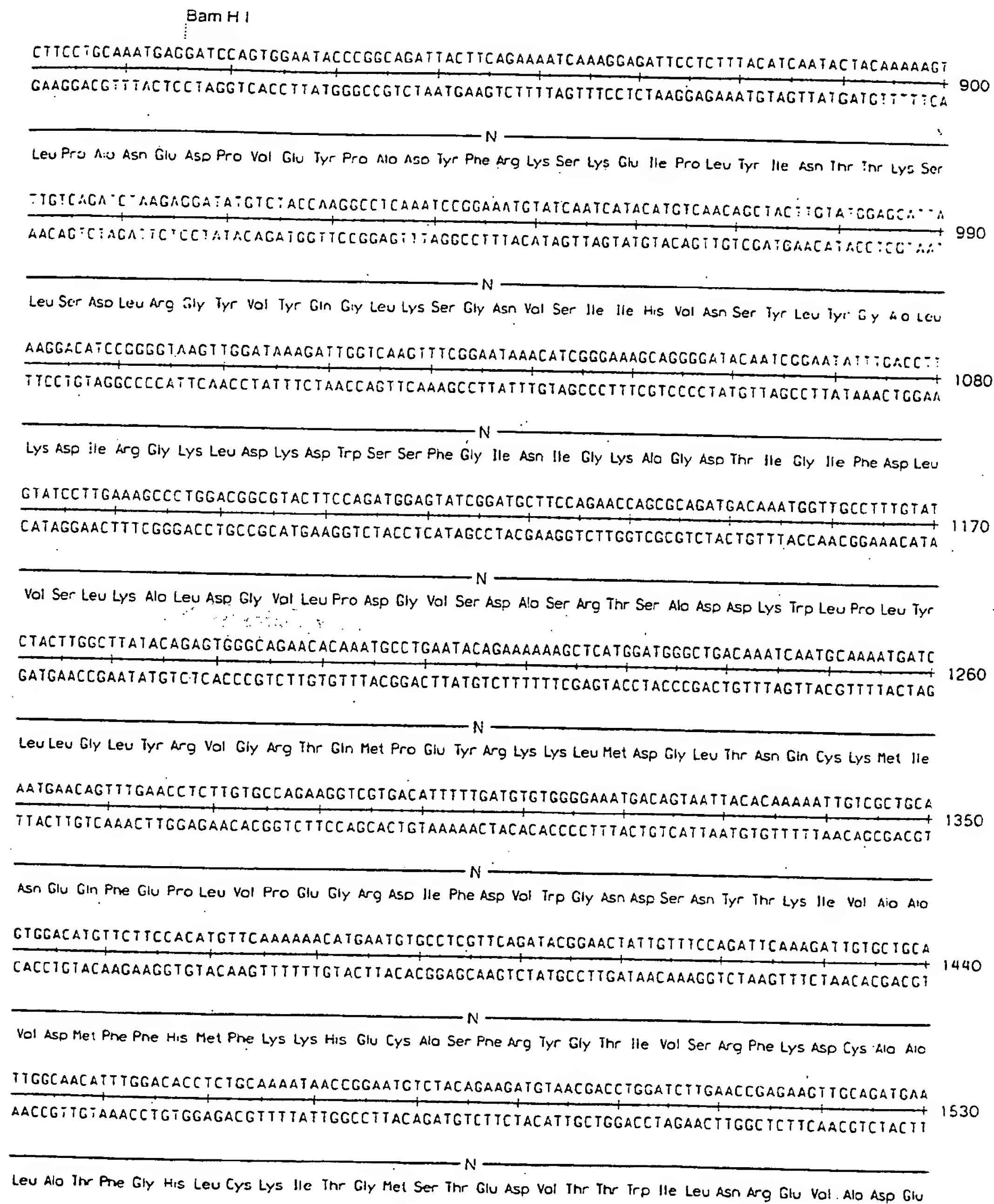
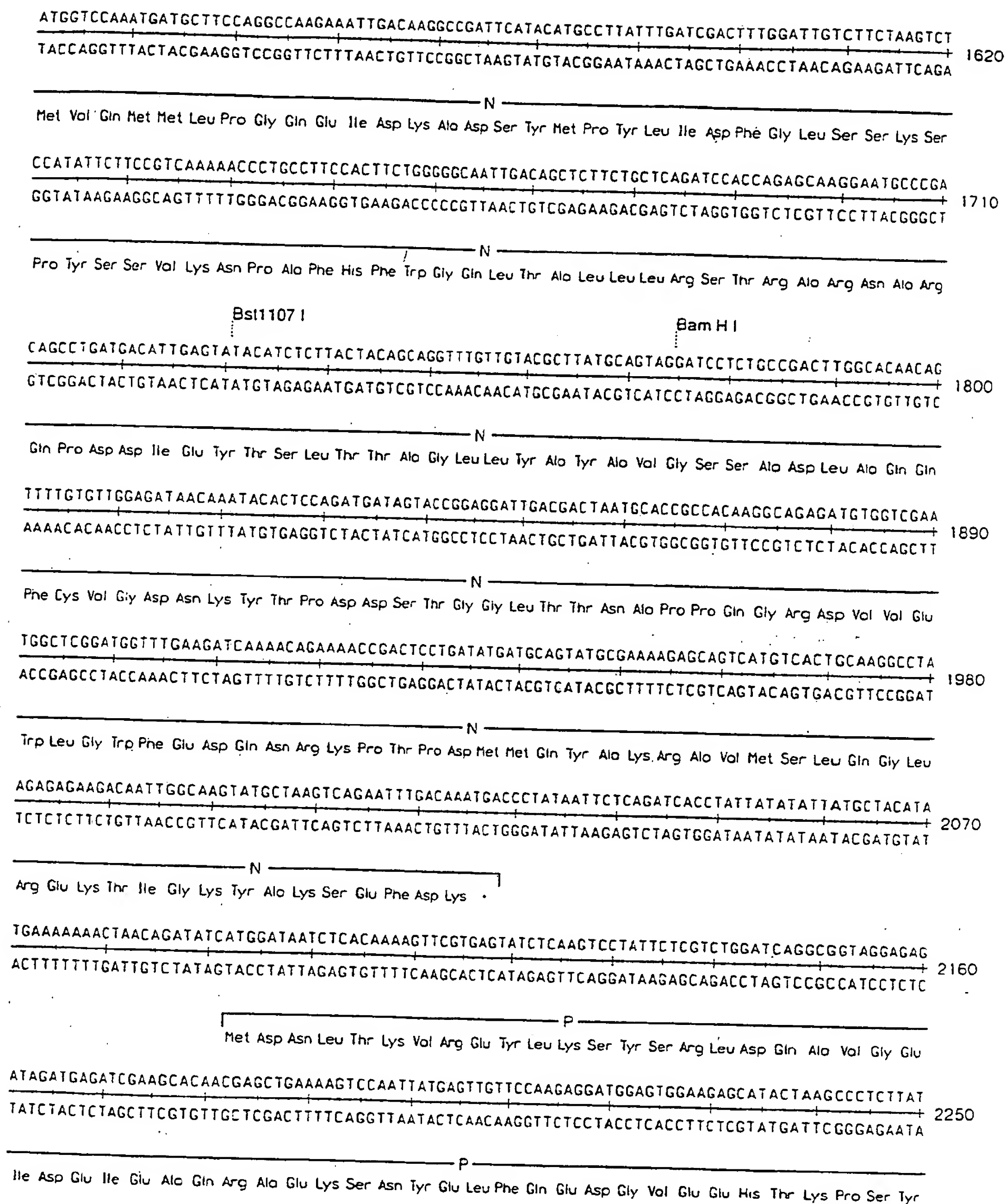
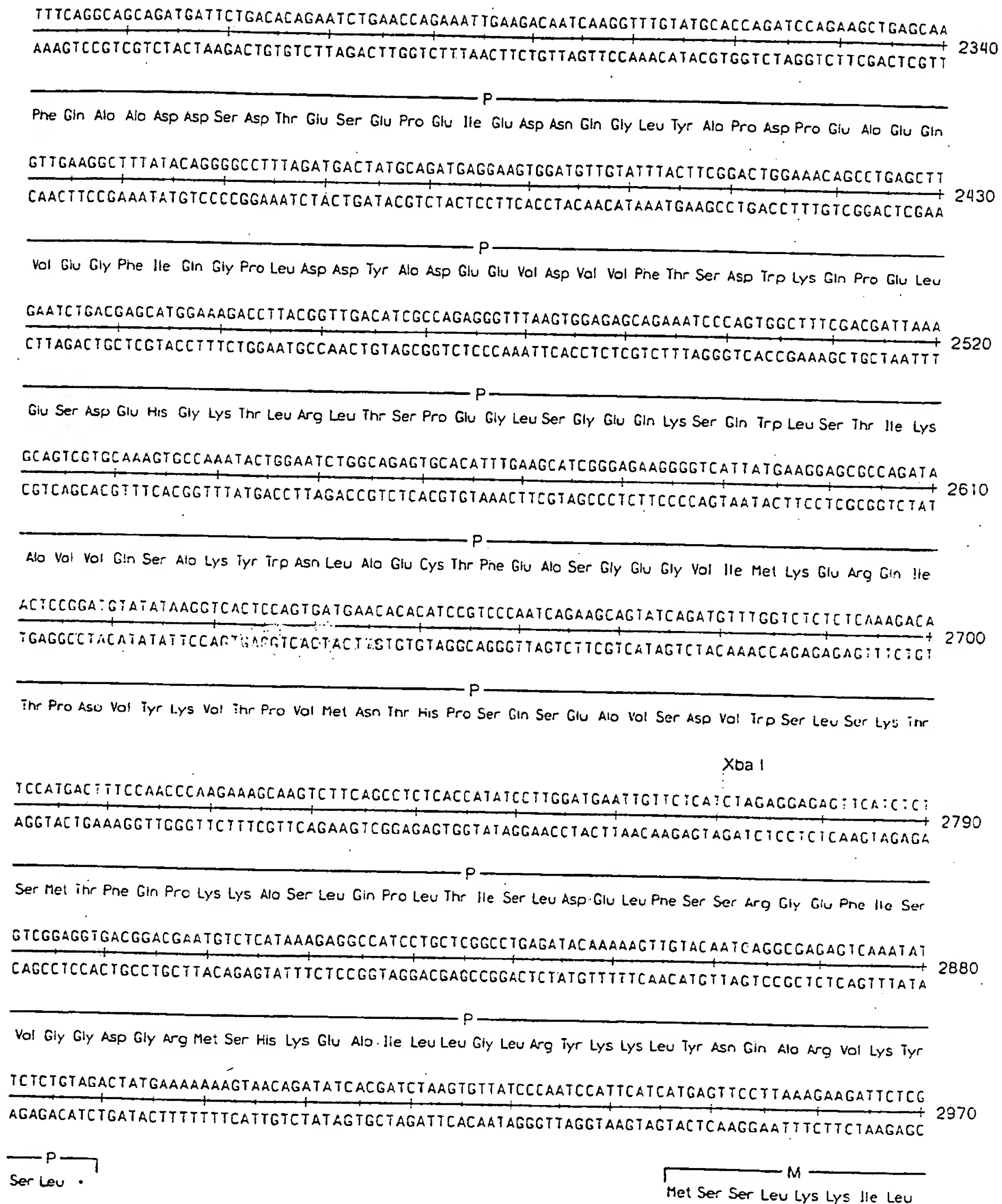
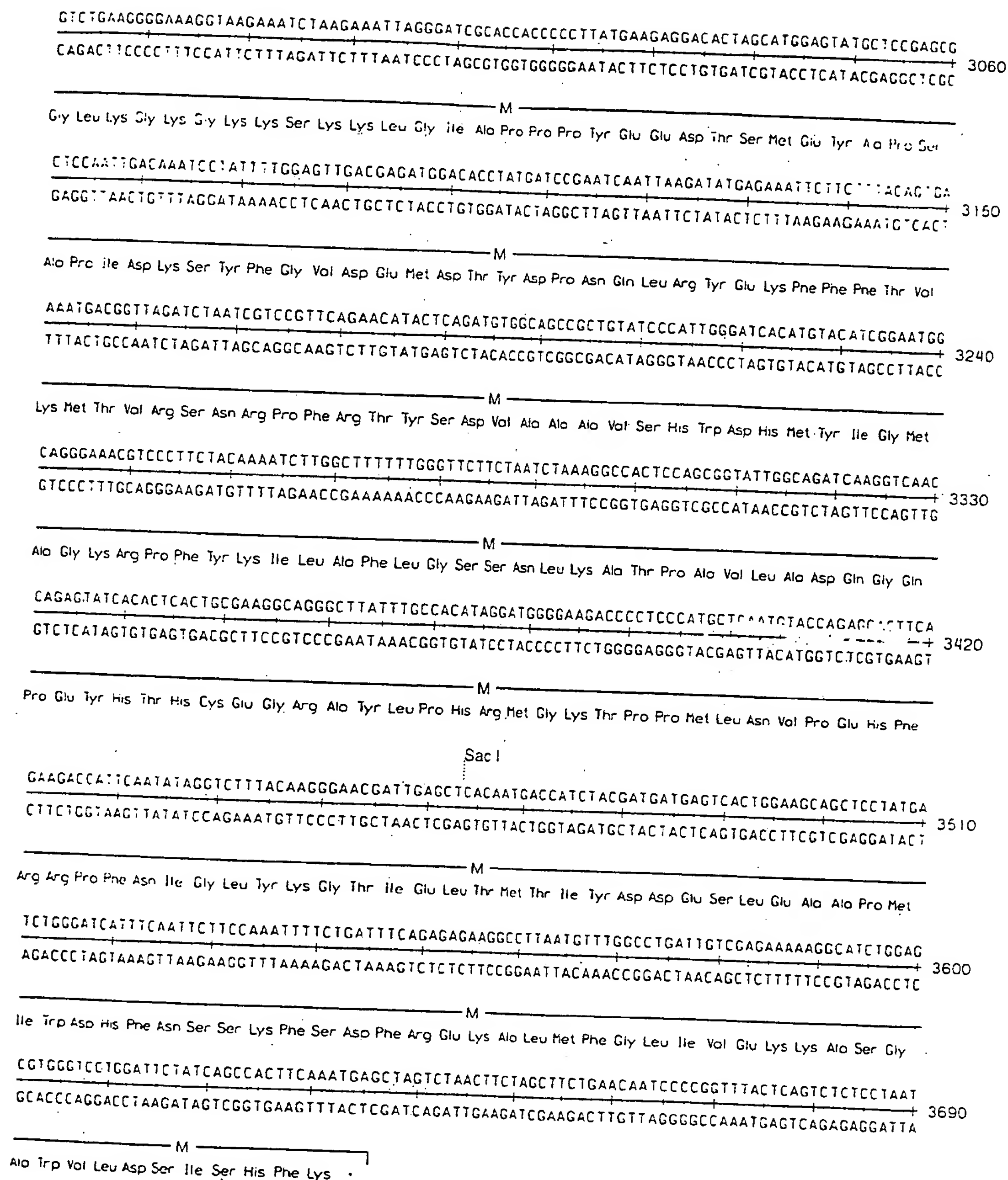
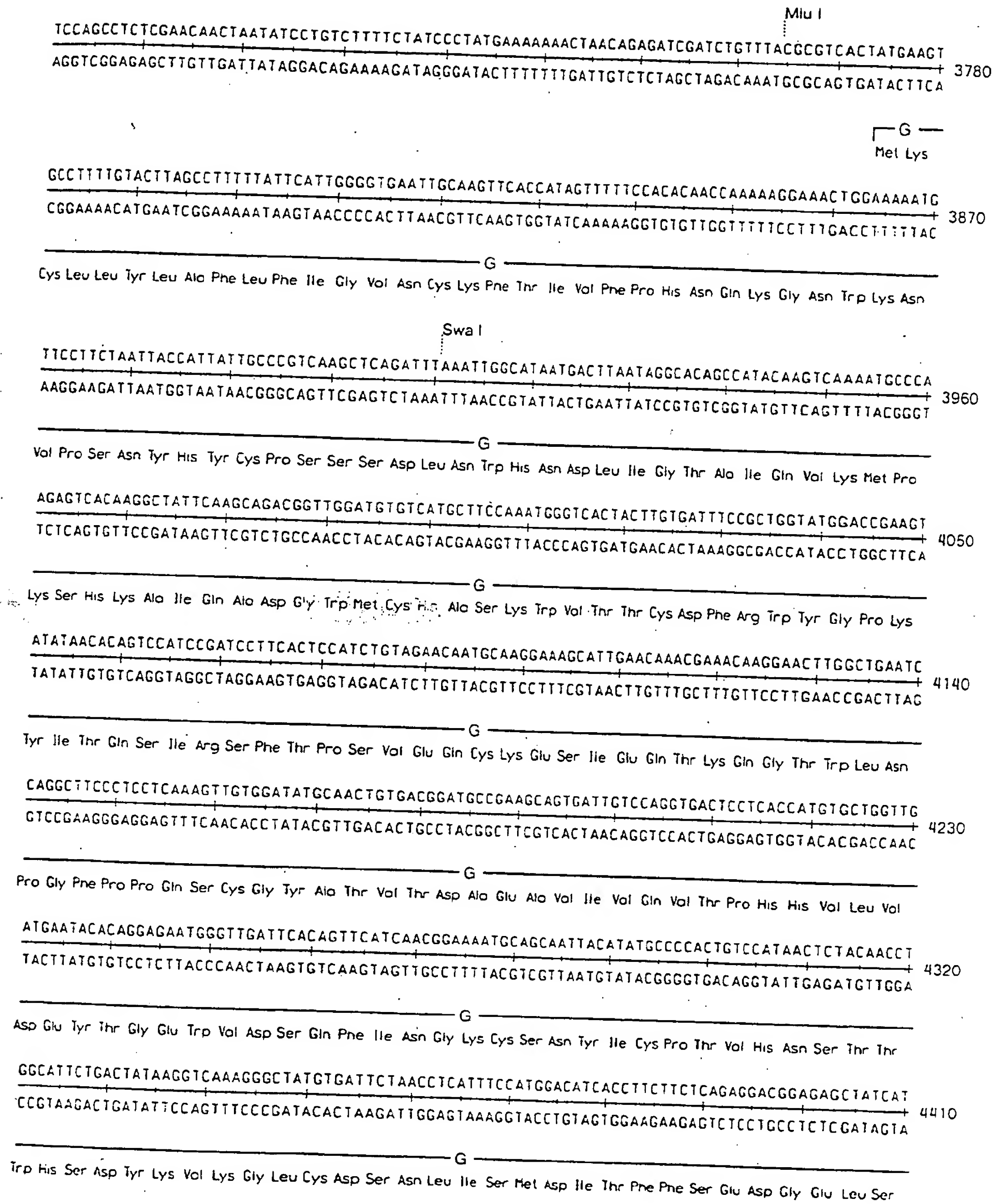


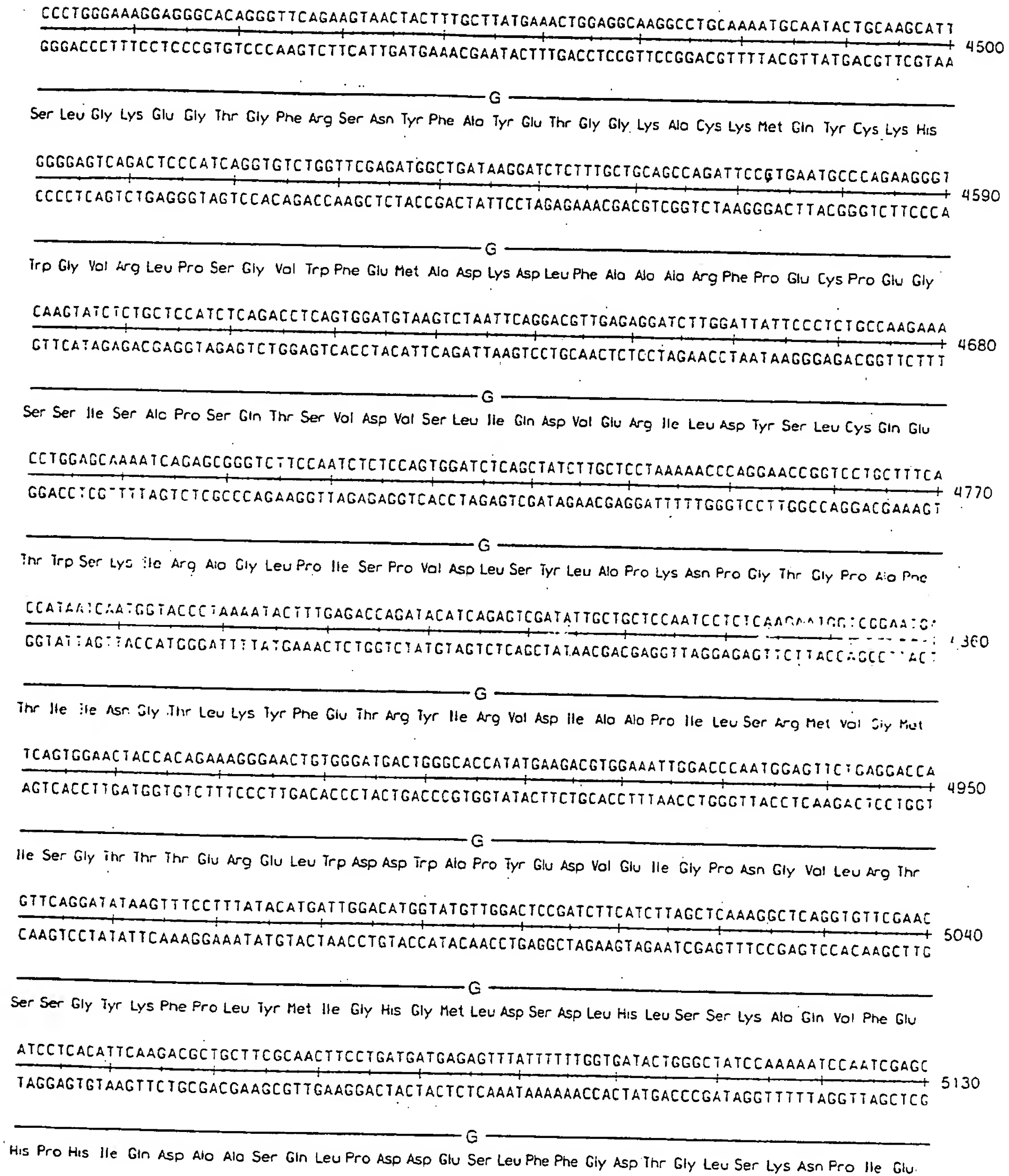
FIG. 1 (CONT.)

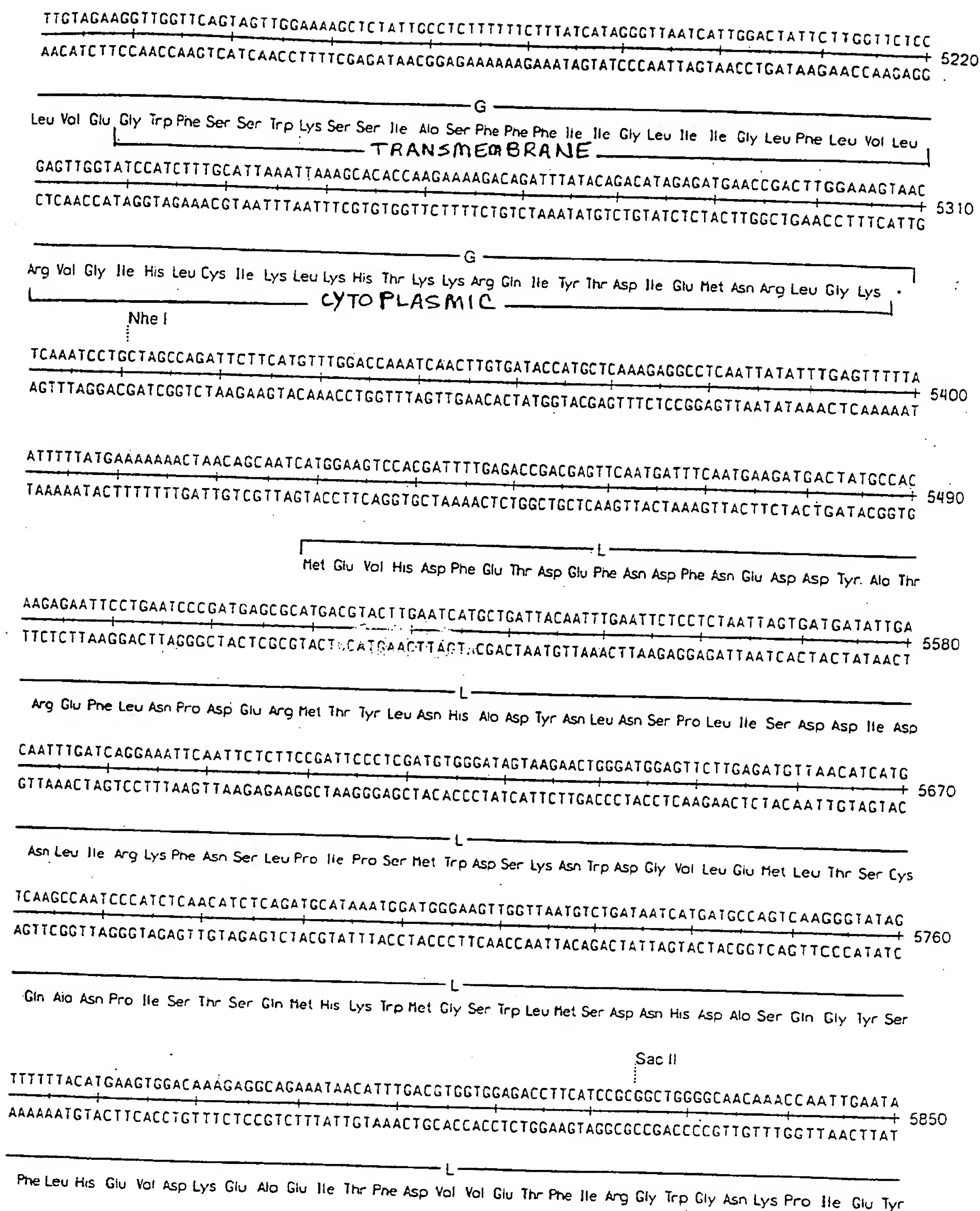












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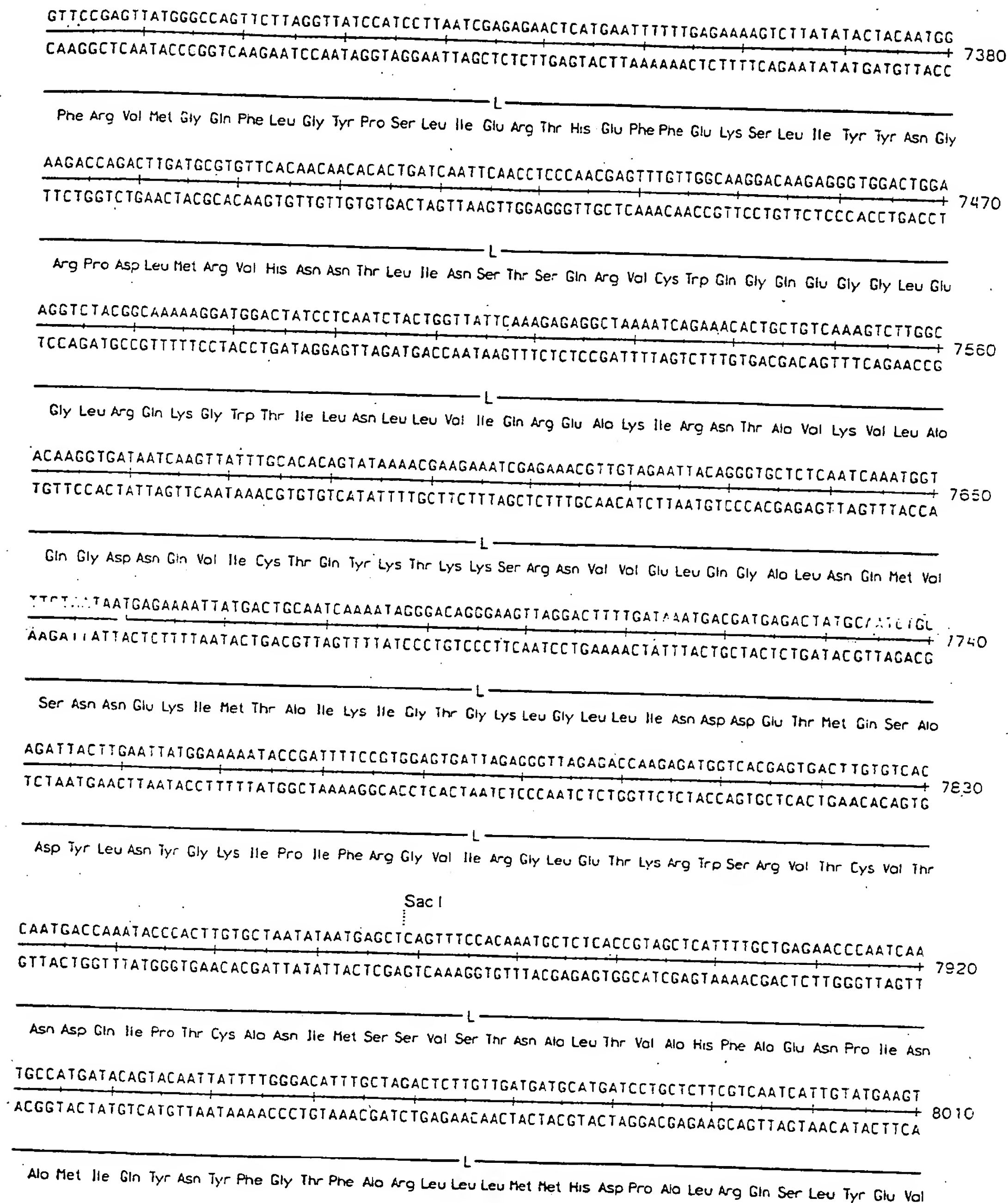
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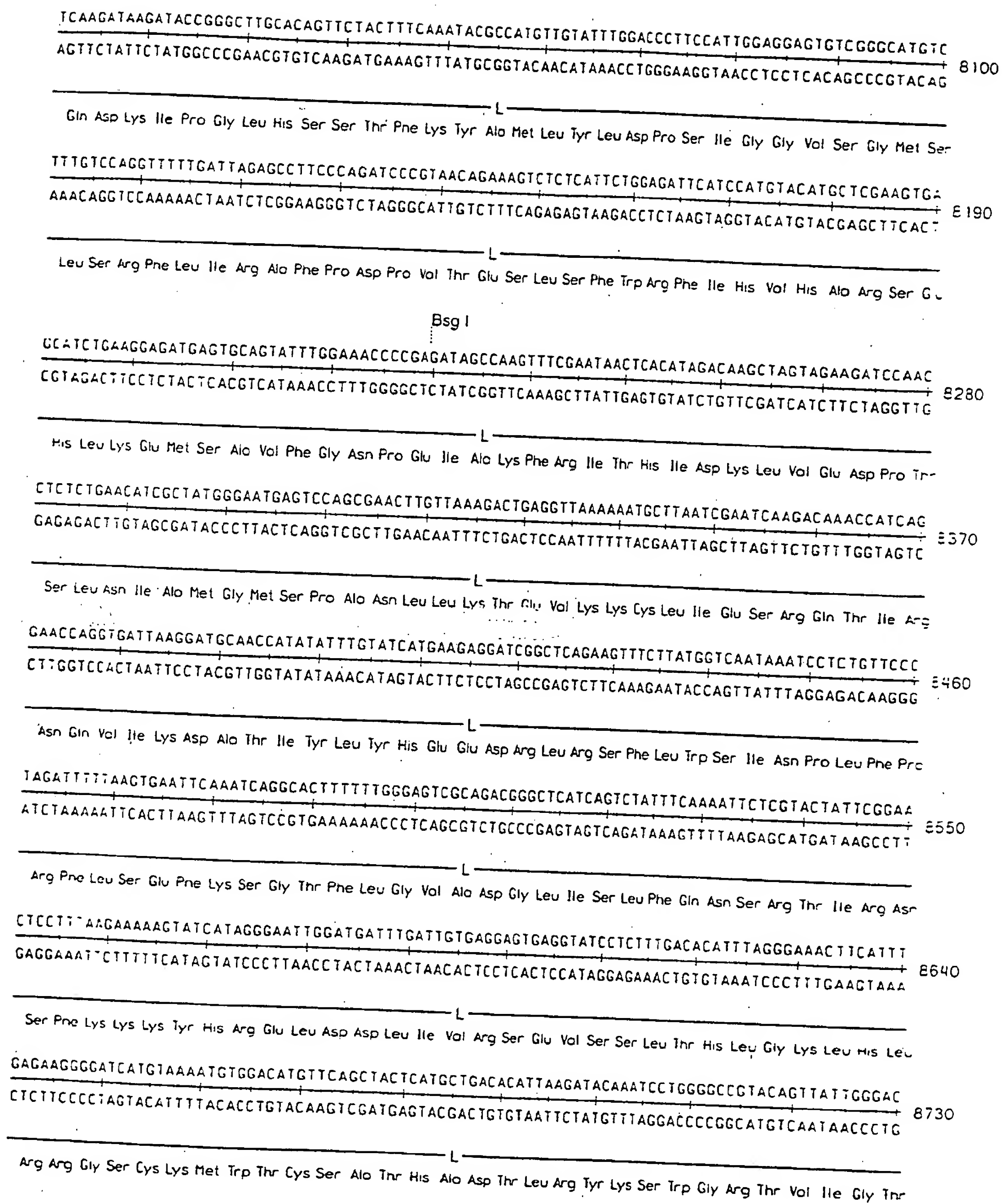
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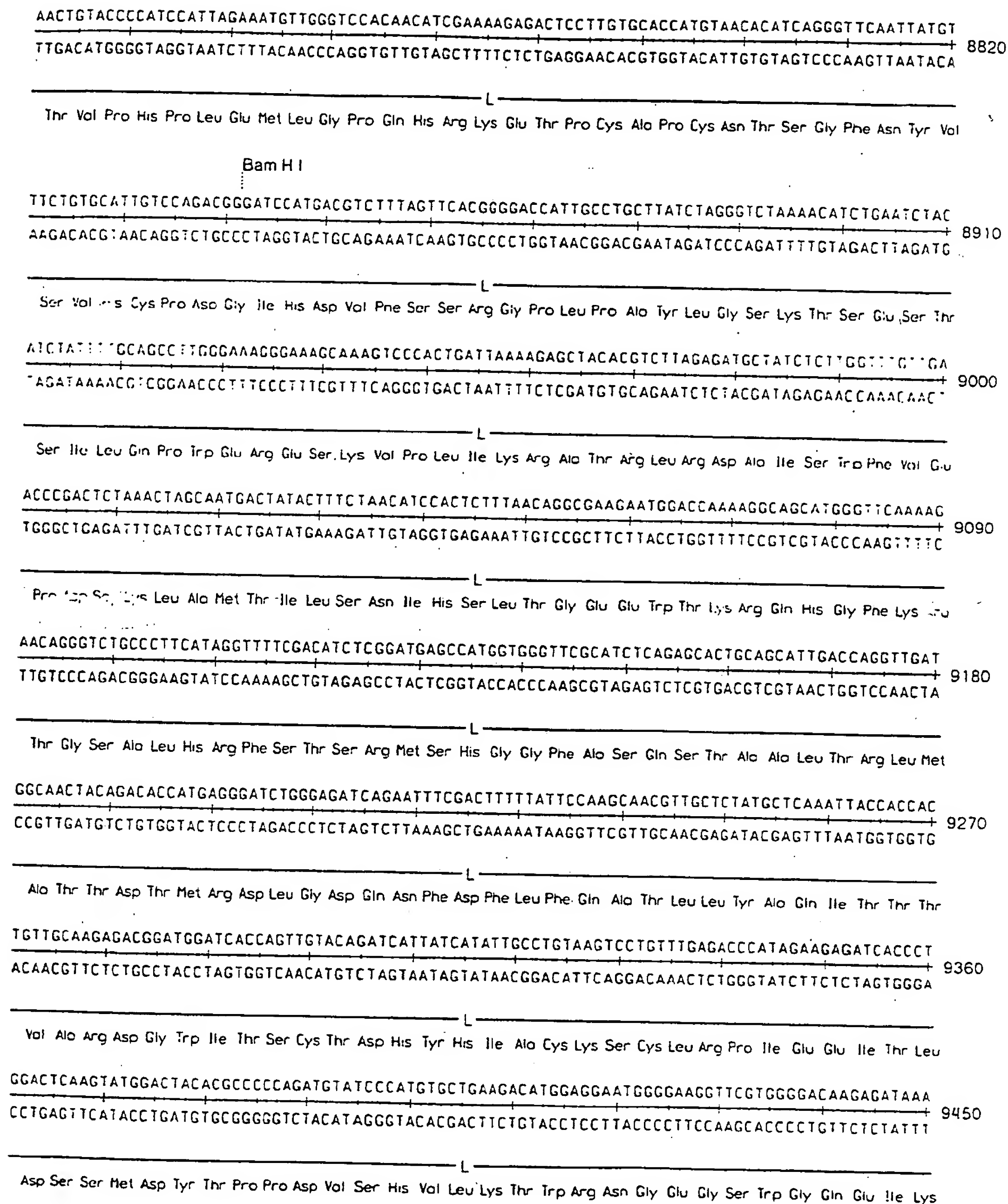
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Sal I

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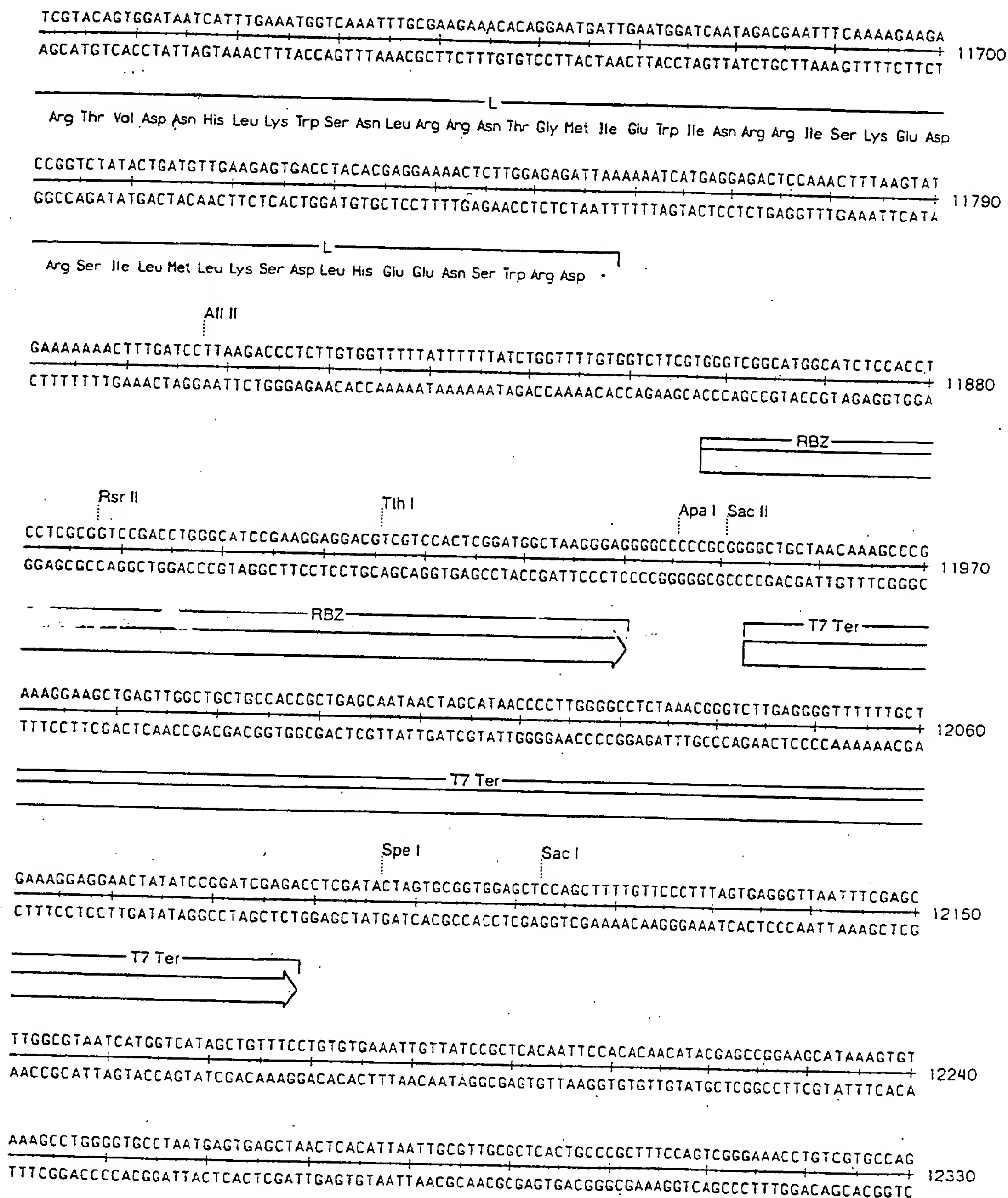
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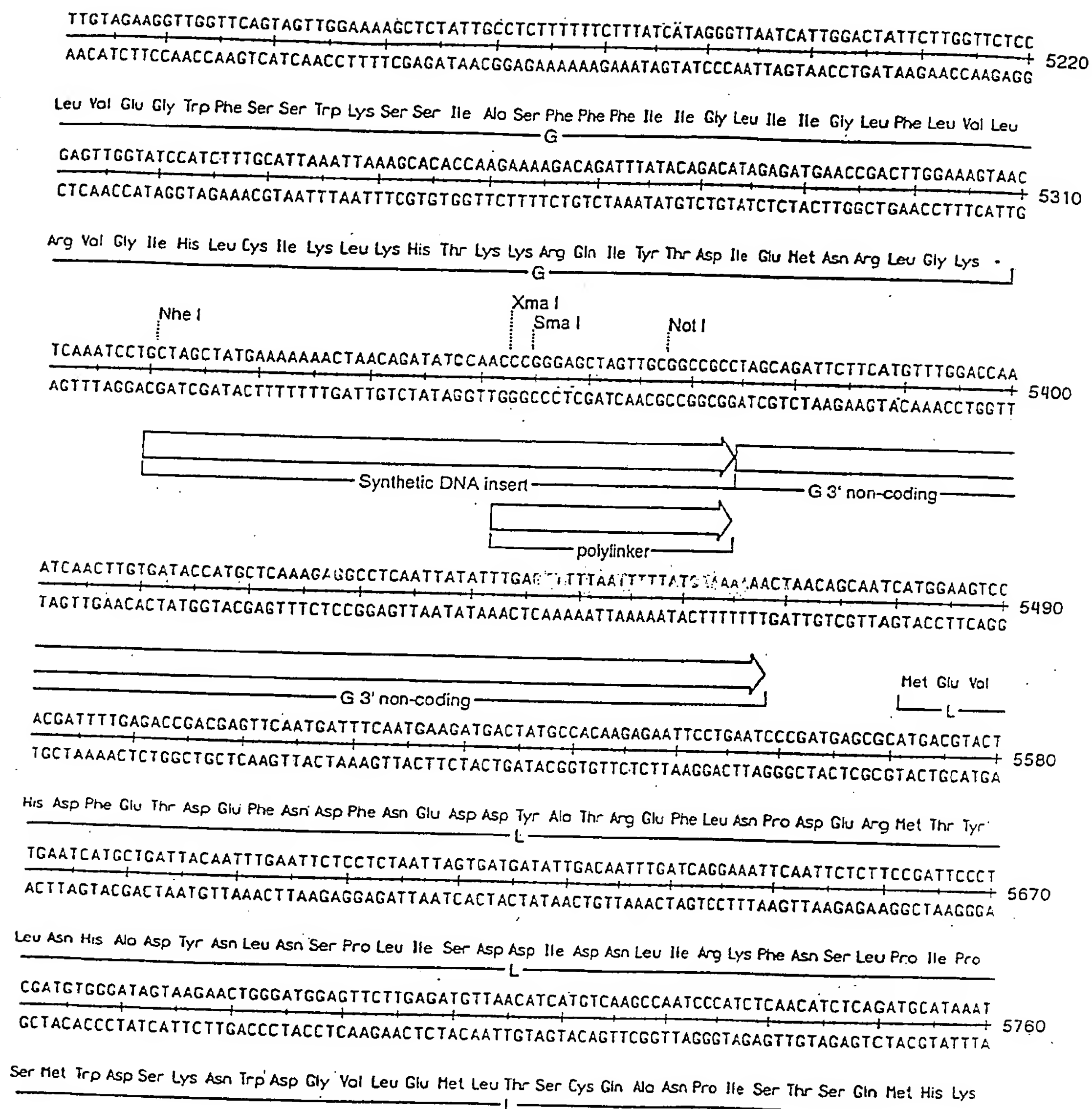
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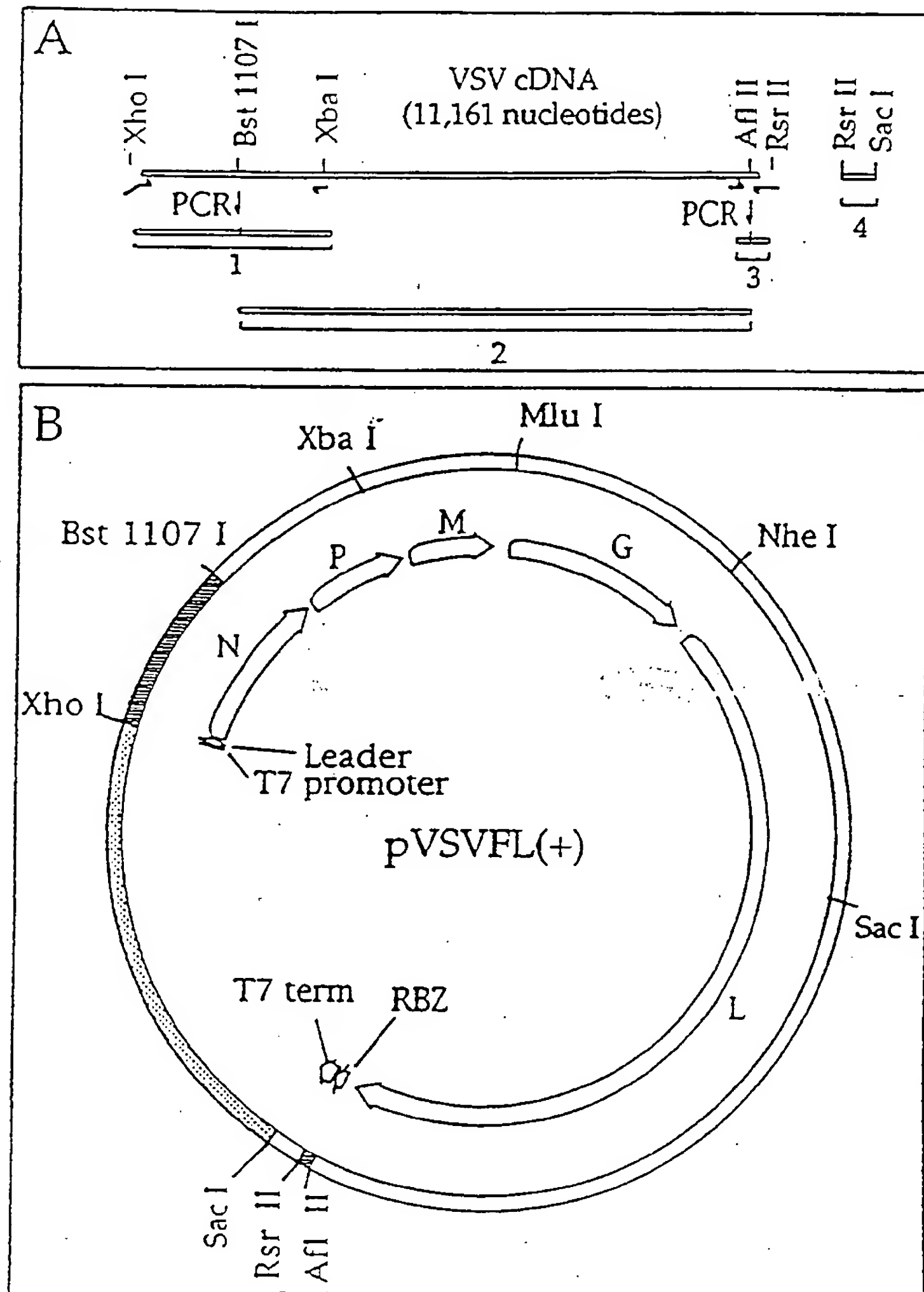
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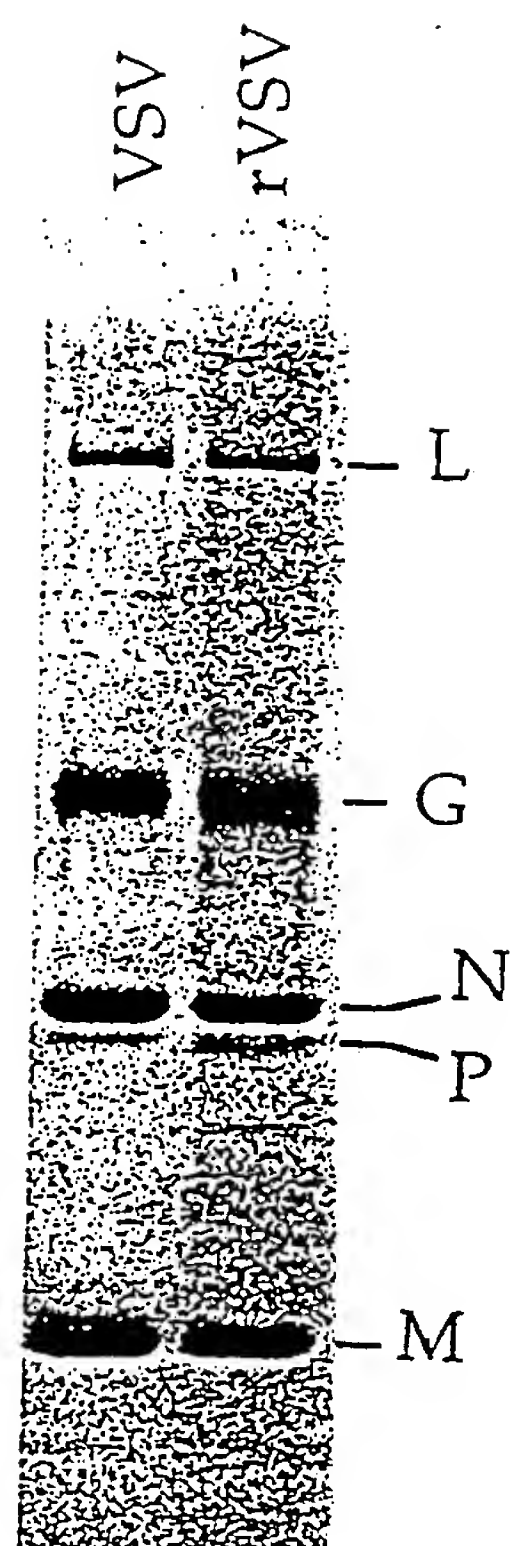
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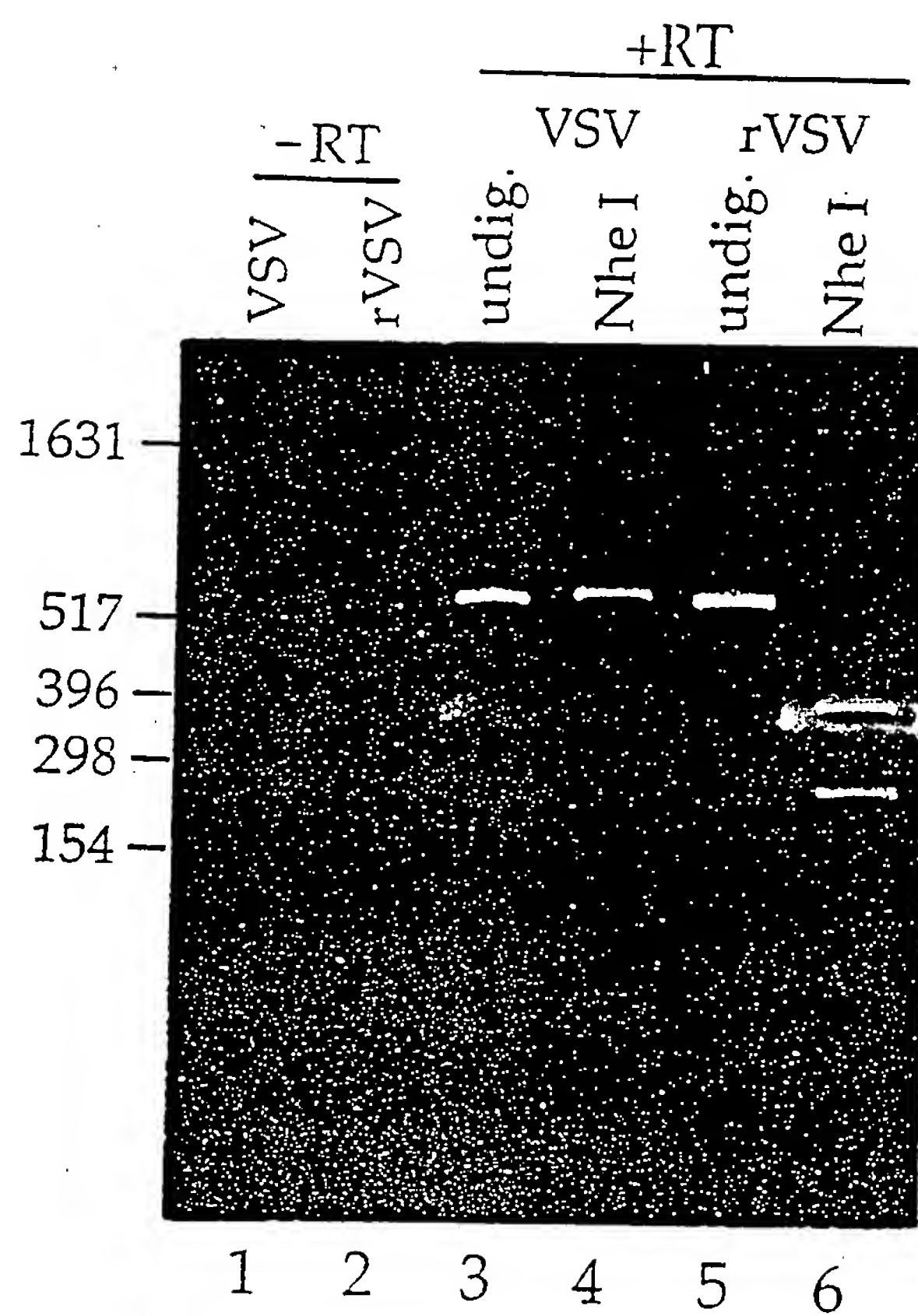
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mRNAs	5' ... GUAGACUAUG · poly(A) ^{NS} ^G _{PPP} ^M AACAGUAUC ... 3'	21, 22
vRNA	3' ... CAUCUGAUACUUUUUUUGAUUGUCUAUAG ... 5'	23
mRNAs	5' ... UAUCCCUAUG · poly(A) ^M ^G _{PPP} ^G AACAGAGAUC ... 3'	24, 25
vRNA	3' ... AUAGGGAUACUUUUUUUGAUUGUCUCUAG ... 5'	26
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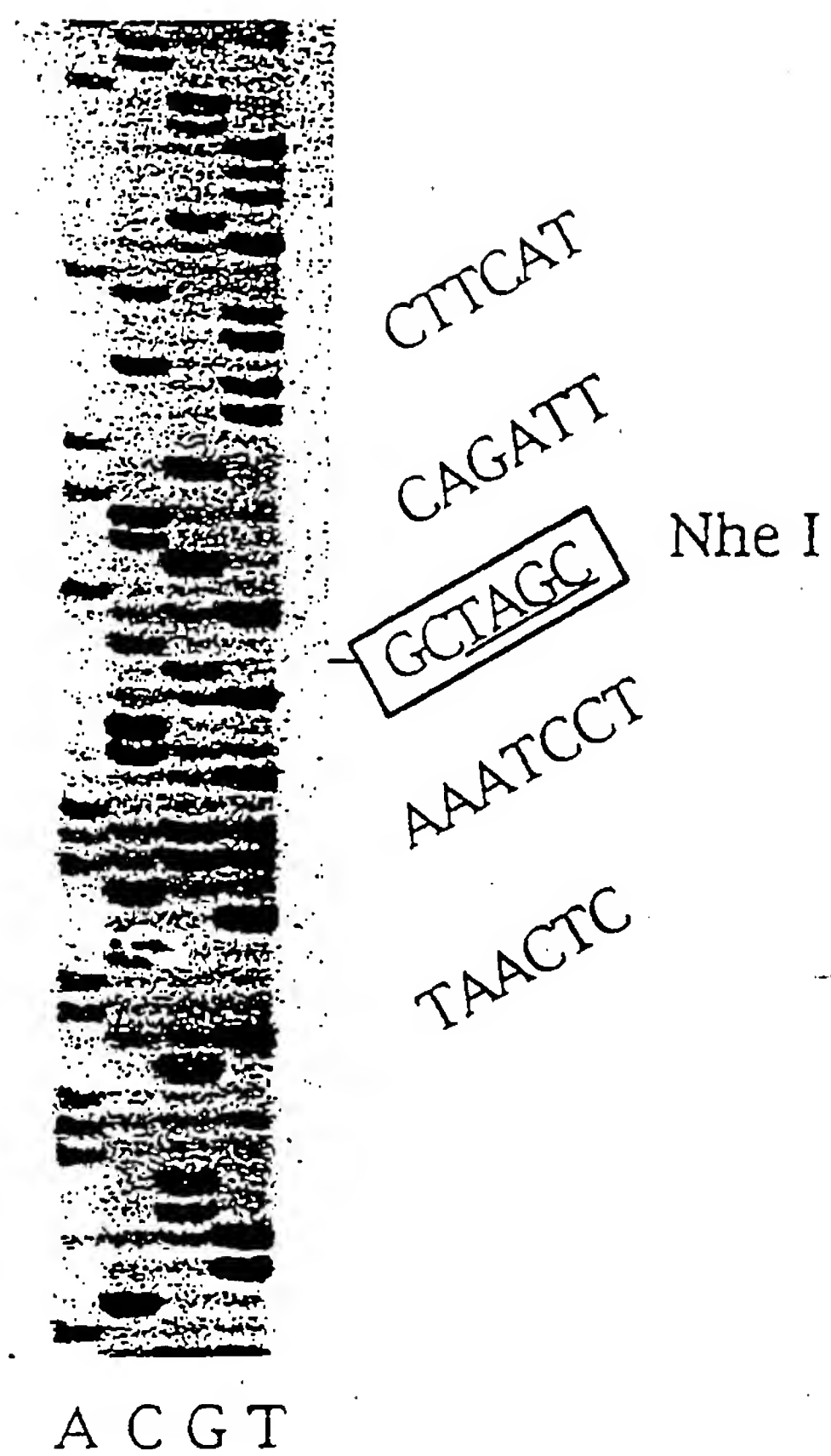
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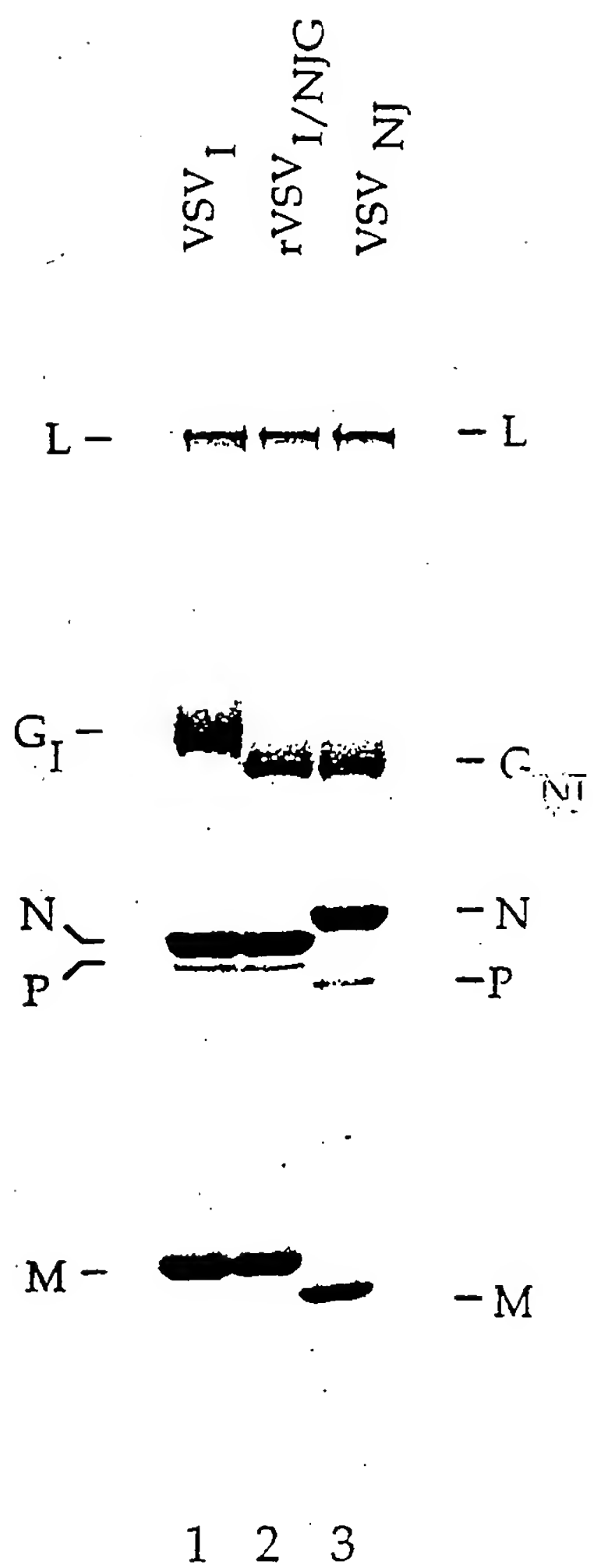
FIG. 5



24/26

FIG. 6





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FIG. 8

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US96/06053

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) : Please See Extra Sheet.

US CL : Please See Extra Sheet.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : Please See Extra Sheet.

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

APS, DIALOG (BIOSIS, DISSABS, EMBASE, MEDLINE, WPIDS)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	US 5,166,057 A (PALESE et al.) 24 November 1992 (24/11/92), see entire document.	1-74
Y	SCHNELL et al. Infectious rabies viruses from cloned cDNA. The EMBO Journal. 1994, Vol. 13, No. 18, pages 4195-4203, see entire article	1-74
Y	OWENS et al. Cytoplasmic domain requirement for incorporation of a foreign envelope protein into Vesicular Stomatitis Virus. Journal of Virology. January 1993, Vol. 67, No. 1, pages 360-365, especially abstract and discussion.	1-74

☒ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:	"T"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"A" document defining the general state of the art which is not considered to be of particular relevance		
"E" earlier document published on or after the international filing date	"X"	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Y"	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"O" document referring to an oral disclosure, use, exhibition or other means		
"P" document published prior to the international filing date but later than the priority date claimed	"&"	document member of the same patent family

Date of the actual completion of the international search

27 JUNE 1996

Date of mailing of the international search report

01 AUG 1996

Name and mailing address of the ISA/US
Commissioner of Patents and Trademarks
Box PCT
Washington, D.C. 20231

Facsimile No. (703) 305-3230

Authorized officer

PHUONG BUI

Telephone No. (703) 308-0196

Form PCT/ISA/210 (second sheet)(July 1992)*

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US96/06053

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	SEONG, B.L. Influencing the Influenza Virus: Genetic Analysis and Engineering of the Negative-Sense RNA genome. Infectious Agents and Disease. 1993, Vol. 2, No. 1, pages 17-24, see entire article, especially conclusions, first paragraph, last sentence.	1-74
A	WHELAN et al. Efficient recovery of infectious vesicular stomatitis virus entirely from cDNA clones. Proc. Natl. Acad. Sci. USA. August 1995, Vol. 92, pages 8388-8392, see entire article.	1-74
A	COLLINS et al. Production of infectious human respiratory syncytial virus from cloned cDNA confirms an essential role for the transcription elongation factor from the 5' proximal open reading frame of the M2 mRNA in gene expression and provides a capability for vaccine development. Proc. Natl. Acad. Sci. USA. December 1995, Vol. 92, pages 11563-11567, see entire article.	1-74

Form PCT/ISA/210 (continuation of second sheet)(July 1992)*

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US96/06053

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

Please See Extra Sheet.

1. ☒ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

Form PCT/ISA/210 (continuation of first sheet(1))(July 1992)★

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US96/06053

A. CLASSIFICATION OF SUBJECT MATTER: IPC (6):

A61K 39/205
C07H 21/02, 21/04
C12N 5/10, 5/47, 7/01, 7/04, 15/01, 15/47, 15/63, 15/86
C12P 21/00

A. CLASSIFICATION OF SUBJECT MATTER: US CL :

424/199.1, 224.1,
435/69.3, 172.3, 235.1, 236, 239, 240.2, 320.1, 810
536/23.72

B. FIELDS SEARCHED Minimum documentation searched Classification System: U.S.

424/199.1, 224.1,
435/69.3, 172.3, 235.1, 236, 239, 240.2, 320.1
536/23.72

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING This ISA found multiple inventions as follows:

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees must be paid.

I. Claims 1-10, 13-36, 39-43 and 51-59, drawn to recombinant vesiculoviruses, host cells, a first method of making recombinant vesiculoviruses, and a first method of using recombinant vesiculoviruses.

II. Claims 11-12, drawn to a second product, directed to a plasmid and a nucleic acid sequence.

III. Claims 37-38, drawn to a third product, directed to combination vaccines.

IV. Claims 44-50, drawn to a fourth product, directed to kits containing nucleic acids.

V. Claims 60-72, drawn to a fifth product, directed to inactivated vesiculoviruses, vaccines, kit and method of use.

VI. Claim 73, drawn to a second method, directed to a method of making viral proteins.

VII. Claim 74, drawn to a third method, directed to a method of making an inactivated vaccine.

The inventions listed as Groups I-VII do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons:

Inventions VII and V are related as process of making and product made. The inactivated vesiculoviruses of the claimed invention can be produced by using a variety of inactivating agents such as radiation, mutagenizing chemicals, or site-directed mutagenesis and are not so linked by special technical feature within the meaning of PCT Rule 13.2 so as to form a single general inventive concept.

Further, the products of Groups I, II, III, IV, and V differ one from another in their physical, chemical, and immunological properties such as chemical structure and composition, primary amino acid or nucleotide sequence, and antigenicity and immunogenicity and are not so linked by special technical feature within the meaning of PCT Rule 13.2 so as to form a single general inventive concept.

Further, the methods of Groups I, V, VI, and VII each differ one from another in method steps, reagents, and utility and are not so linked by special technical feature within the meaning of PCT Rule 13.2 so as to form a single general inventive concept.

Further, the products of groups I through IV and the methods of groups VI and VII are directed to independent inventions not so linked by special technical feature within the meaning of PCT Rule 13.2 so as to form a single general inventive concept.

**CORRECTED
VERSION***

PCT

WORLD INTELLECTUAL PROPERTY ORGANIZATION
International Bureau



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : A61K 39/205, C07H 21/02, 21/04, C12N 5/10, 5/47, 7/01, 7/04, 15/01, 15/47, 15/63, 15/86, C12P 21/00		A1	(11) International Publication Number: WO 96/34625 (43) International Publication Date: 7 November 1996 (07.11.96)
(21) International Application Number: PCT/US96/06053 (22) International Filing Date: 1 May 1996 (01.05.96) (30) Priority Data: 435,032 4 May 1995 (04.05.95) US (60) Parent Application or Grant (63) Related by Continuation US 435,032 (CIP) Filed on 4 May 1995 (04.05.95) (71) Applicant (for all designated States except US): YALE UNIVERSITY [US/US]; 451 College Street, New Haven, CT 06520 (US). (72) Inventor; and (75) Inventor/Applicant (for US only): ROSE, John, K. [US/US]; 21 Shell Beach Road, Guilford, CT 06437 (US). (74) Agents: MISROCK, S., Leslie et al.; Pennie & Edmonds, 1155 Avenue of the Americas, New York, NY 10036 (US).		(81) Designated States: AL, AM, AU, AZ, BB, BG, BR, BY, CA, CN, CZ, EE, FI, GE, HU, IS, JP, KG, KP, KR, KZ, LK, LR, LS, LT, LV, MD, MG, MK, MN, MX, NO, NZ, PL, RO, RU, SG, SI, SK, TJ, TM, TR, TT, UA, US, UZ, VN, ARIPO patent (KE, LS, MW, SD, SZ, UG), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG). Published With international search report.	
(54) Title: RECOMBINANT VESICULOVIRUSES AND THEIR USES			
(57) Abstract <p>The present invention provides recombinant replicable vesiculoviruses. The invention provides a method which, for the first time, successfully allows the production and recovery of replicable vesiculoviruses, as well as recombinant replicable vesiculoviruses, from cloned DNA, by a method comprising expression of the full-length positive-strand vesiculovirus antigenomic RNA in host cells. The recombinant vesiculoviruses do not cause serious pathology in humans, can be obtained in high titers, and have use as vaccines. The recombinant vesiculoviruses can also be inactivated for use as killed vaccines.</p>			

* (Referred to in PCT Gazette No. 04/1997, Section II)

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

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FI	Finland	MN	Mongolia	US	United States of America
FR	France	MR	Mauritania	UZ	Uzbekistan
GA	Gabon			VN	Viet Nam

RECOMBINANT VESICULOVIRUSES AND THEIR USES

This invention was made with government support under grant number R37 AI243245 awarded by the National Institutes of Health. The government has certain rights in the invention.

1. INTRODUCTION

The present invention relates to recombinant vesiculoviruses which are replicable and capable of expressing foreign nucleic acid contained in their genome. Also provided are inactivated forms of the recombinant viruses. The vesiculoviruses are useful in vaccine formulations to prevent or treat various diseases and disorders.

2. BACKGROUND OF THE INVENTION2.1. RHABDOVIRUSES

Rhabdoviruses are membrane-enveloped viruses that are widely distributed in nature where they infect vertebrates, invertebrates, and plants. There are two distinct genera within the rhabdoviruses, the Lyssavirus genus and the Vesiculovirus genus. Rhabdoviruses have single, negative-strand RNA genomes of 11-12,000 nucleotides (Rose and Schubert, 1987, Rhabdovirus genomes and their products, in *The Viruses: The Rhabdoviruses*, Plenum Publishing Corp., NY, pp. 129-166). The virus particles contain a helical, nucleocapsid core composed of the genomic RNA and protein. Generally, three proteins, termed N (nucleocapsid), P (formerly termed NS, originally indicating nonstructural), and L (large) are found to be associated with the nucleocapsid. An additional matrix (M) protein lies within the membrane envelope, perhaps interacting both with the membrane and the nucleocapsid core. A single glycoprotein (G) species spans the membrane and forms the spikes on the surface of the virus particle. Because the genome is the negative sense [i.e., complementary to the RNA

sequence (positive sense) that functions as mRNA to directly produce encoded protein], rhabdoviruses must encode and package an RNA-dependent RNA polymerase in the virion (Baltimore et al., 1970, Proc. Natl. Acad. Sci. USA 66: 572-576), composed of the P and L proteins. This enzyme transcribes genomic RNA to make subgenomic MRNAs encoding the 5-6 viral proteins and also replicates full-length positive and negative sense RNAs. The genes are transcribed sequentially, starting at the 3' end of the genomes. The same basic genetic system is also employed by the paramyxoviruses and filoviruses.

The prototype rhabdovirus, vesicular stomatitis virus (VSV), grows to very high titers in most animal cells and can be prepared in large quantities. As a result, VSV has been widely used as a model system for studying the replication and assembly of enveloped RNA viruses. The study of VSV and related negative strand viruses has been limited by the inability to perform direct genetic manipulation of the virus using recombinant DNA technology. The difficulty in generating VSV from DNA is that neither the full-length genomic nor antigenomic RNAs are infectious. The minimal infectious unit is the genomic RNA tightly bound to 1,250 subunits of the nucleocapsid (N) protein (Thomas et al., 1985, J. Virol. 54:598-607) and smaller amounts of the two virally encoded polymerase subunits, L and P. To reconstitute infectious virus from the viral RNA, it is necessary first to assemble the N protein-RNA complex that serves as the template for transcription and replication by the VSV polymerase. Although smaller negative-strand RNA segments of the influenza virus genome can be packaged into nucleocapsids *in vitro*, and then rescued in influenza infected cells (Enami et al., 1990, Proc. Natl. Acad. Sci. USA 87:3802-3805; Luytjes et al., 1989, Cell 59:1107-1113), systems for packaging the much larger rhabdoviral genomic RNAs *in vitro* are not yet available.

Recently, systems for replication and transcription of DNA-derived minigenomes or small defective RNAs from

rhabdoviruses (Conzelmann and Schnell, 1994, J. Virol. 68:713-719; Pattnaik et al., 1992, Cell 69:1011-1120) and paramyxoviruses (Calain et al., 1992, Virology 191:62-71; Collins et al., 1991, Proc. Natl. Acad. Sci. USA 88:9663-9667; Collins et al., 1993, Virology 195:252-256; De and Banerjee, 1993, Virology 196:344-348; Dimock and Collins, 1993, J. Virol. 67:2772-2778; Park et al., 1991, Proc. Natl. Acad. Sci. USA 88:5537-5541) have been described. In these systems, RNAs are assembled into nucleocapsids within cells that express the viral N protein and polymerase proteins. Although these systems have been very useful, they do not allow genetic manipulation of the full-length genome of infectious viruses.

The recovery of rabies virus from a complete cDNA clone was published recently (Schnell et al., 1994, EMBO J. 13:4195-4203). The infectious cycle was initiated by expressing the antigenomic (full-length positive strand) RNA in cells expressing the viral N, P, and L proteins. Although rabies virus is a rhabdovirus, it is structurally and functionally different from the vesiculoviruses. Rabies virus is a Lyssavirus, not a Vesiculovirus. Lyssaviruses invade the central nervous system. Vesiculoviruses invade epithelial cells, predominantly those of the tongue, to produce vesicles. Rabies virus causes encephalitis in a variety of animals and in humans, while VSV causes an epidemic but self-limiting disease in cattle. In sharp contrast to VSV-infected cells, rabies virus produces little or no cytopathic effect in infected cell culture, replicates less efficiently than VSV in cell culture, and causes little depression of cellular DNA, RNA or protein synthesis in infected cell cultures (see Baer et al., 1990, in Virology, 2d ed., Fields et al. (eds.), Raven Press, Ltd., NY, pp. 883, 887). Indeed, there is no cross-hybridization observed between the genomes of rabies virus and VSV, and sequence homology between the two genomes is generally discernable only with the aid of computer run homology programs. The differences between vesiculoviruses and rabies virus, and the

extremely rare nature of rabies virus recovery from cDNA (~10⁸ cells are transfected to yield one infectious cell), renders it unpredictable whether the strategy used with rabies virus would be successful for viruses of a different genus, i.e.,
5 the vesiculoviruses.

The recovery of infectious measles virus, another negative strand RNA virus, from cloned cDNA has been attempted, without success (see Ballart et al., 1990, EMBO J. 9(2):379-384 and the retraction thereof by Eschle et al.,
10 1991, EMBO J. 10(11):3558).

2.2. VACCINES

The development of vaccines for the prevention of viral, bacterial, or parasitic diseases is the focus of much
15 research effort.

Traditional ways of preparing vaccines include the use of inactivated or attenuated pathogens. A suitable inactivation of the pathogenic microorganism renders it harmless as a biological agent but does not destroy its
20 immunogenicity. Injection of these "killed" particles into a host will then elicit an immune response capable of preventing a future infection with a live microorganism. However, a major concern in the use of killed vaccines (using inactivated pathogen) is failure to inactivate all the
25 microorganism particles. Even when this is accomplished, since killed pathogens do not multiply in their host, or for other unknown reasons, the immunity achieved is often incomplete, short lived and requires multiple immunizations. Finally, the inactivation process may alter the
30 microorganism's antigens, rendering them less effective as immunogens.

Attenuation refers to the production of strains of pathogenic microorganisms which have essentially lost their disease-producing ability. One way to accomplish this is to
35 subject the microorganism to unusual growth conditions and/or frequent passage in cell culture. Mutants are then selected which have lost virulence but yet are capable of eliciting an

immune response. Attenuated pathogens often make good immunogens as they actually replicate in the host cell and elicit long lasting immunity. However, several problems are encountered with the use of live vaccines, the most worrisome being insufficient attenuation and the risk of reversion to virulence.

An alternative to the above methods is the use of subunit vaccines. This involves immunization only with those components which contain the relevant immunological material.

10 Vaccines are often formulated and inoculated with various adjuvants. The adjuvants aid in attaining a more durable and higher level of immunity using small amounts of antigen or fewer doses than if the immunogen were administered alone. The mechanism of adjuvant action is
15 complex and not completely understood. However, it may involve the stimulation of cytokine production, phagocytosis and other activities of the reticuloendothelial system as well as a delayed release and degradation of the antigen. Examples of adjuvants include Freund's adjuvant (complete or
20 incomplete), Adjuvant 65 (containing peanut oil, mannide monooleate and aluminum monostearate), the pluronic polyol L-121, Avridine, and mineral gels such as aluminum hydroxide, aluminum phosphate, etc. Freund's adjuvant is no longer used in vaccine formulations for humans because it contains
25 nonmetabolizable mineral oil and is a potential carcinogen.

3. SUMMARY OF THE INVENTION

The present invention provides recombinant replicable vesiculoviruses. The prior art has unsuccessfully
30 attempted to produce replicable vesiculoviruses from cloned DNA. In contrast, the invention provides a method which, for the first time, has successfully allowed the production and recovery of replicable vesiculoviruses, as well as recombinant replicable vesiculoviruses, from cloned DNA.

35 The vesiculoviruses of the invention are produced by providing in an appropriate host cell: (a) DNA that can be transcribed to yield (encodes) vesiculovirus antigenomic

(+) RNA (complementary to the vesiculovirus genome), (b) a recombinant source of vesiculovirus N protein, (c) a recombinant source of vesiculovirus P protein, and (d) a recombinant source of vesiculovirus L protein; under
5 conditions such that the DNA is transcribed to produce the antigenomic RNA, and a vesiculovirus is produced that contains genomic RNA complementary to the antigenomic RNA produced from the DNA.

The invention provides an infectious recombinant
10 vesiculovirus capable of replication in an animal into which the recombinant vesiculovirus is introduced, in which the genome of the vesiculovirus comprises foreign RNA which is not naturally a part of the vesiculovirus genome. The recombinant vesiculovirus is formed by producing
15 vesiculoviruses according to the method of the invention, in which regions of the DNA encoding vesiculovirus antigenomic (+) RNA that are nonessential for viral replication have been inserted into or replaced with foreign DNA.

In a preferred embodiment, the foreign RNA
20 contained within the genome of the recombinant vesiculovirus (originally encoded by the foreign DNA), upon expression in an appropriate host cell, produces a protein or peptide that is antigenic or immunogenic.

The recombinant vesiculoviruses of the invention
25 have use as vaccines. In one embodiment, where the foreign RNA directs production of an antigen that induces an immune response against a pathogen, the vaccines of the invention have use in the treatment or prevention of infections by such a pathogen (particularly a pathogenic microorganism), and its
30 clinical manifestations, i.e., infectious disease. In a preferred embodiment, such an antigen displays the antigenicity or immunogenicity of an envelope glycoprotein of a virus other than a vesiculovirus, and the antigen is incorporated into the vesiculovirus envelope. The
35 recombinant vesiculoviruses also have uses in diagnosis, and monitoring progression of infectious disorders, including response to vaccination and/or therapy.

In another embodiment, where the foreign RNA directs production of an antigen that induces an immune response against a tumor, the recombinant viruses of the invention have uses in cancer immunoprophylaxis, immunotherapy, and diagnosis, and monitoring of tumor progression or regression.

The recombinant vesiculoviruses can be used as live vaccines, or can be inactivated for use as killed vaccines. The recombinant viruses can also be used to produce large quantities of readily purified antigen, e.g., for use in subunit vaccines.

The invention also provides vaccine formulations, kits, and recombinant host cells.

15

4. DESCRIPTION OF THE FIGURES

Figure 1. Nucleotide sequence of plasmid pVSVFL(+), showing the complete DNA sequence that is transcribed to produce VSV antigenomic (+) RNA, and predicted sequences of the encoded VSV proteins. [N protein: SEQ ID NO:2; P protein: SEQ ID NO:3; M protein: SEQ ID NO:4; G protein: SEQ ID NO:5; L protein: SEQ ID NO:6] The noncoding and intergenic regions are observable. The upper line of sequence (SEQ ID NO:1) is the VSV antigenomic positive strand; lower line = SEQ ID NO:7. Restriction sites are indicated. The transmembrane and cytoplasmic domains of the G protein are also indicated. The sequences of the first T7 RNA polymerase promoter (SEQ ID NO:8), the second T7 RNA polymerase promoter (SEQ ID NO:9); leader sequence (SEQ ID NO:10), T7 RNA polymerase transcription termination signal (SEQ ID NO:11), and the sequence that is transcribed to produce the HDV ribozyme (SEQ ID NO:12) are shown.

Figure 2. Nucleotide sequence of a portion of plasmid pVSVSS1, showing the synthetic DNA insert containing the polylinker region inserted between the G and L coding regions (3' of G and 5' of L) containing unique restriction enzyme recognition sites, namely, XmaI, NotI, and SmaI.

Upper line of sequence: SEQ ID NO:13; lower line of sequence: SEQ ID NO:14.

Figure 3. Gene junctions of VSV. The nucleotide sequences at the 3' end of the leader RNA and the 5' and 3' ends of each mRNA are shown along with the corresponding genomic sequences (vRNA) (SEQ ID NO:15-31). The intergenic dinucleotides are indicated by bold letters. From Rose and Schubert, 1987, in *The Viruses: The Rhabdoviruses*, Plenum Press, NY, pp. 129-166, at p. 136.

10 Figure 4. Plasmid DNA construction. A. The diagram illustrates the cloned VSV genomic sequence and the four DNA fragments (numbered 1-4) that were used to generate the plasmid pVSVFL(+). The horizontal arrows represent PCR primers used to generate fragments 1 and 3. B. Diagram of
15 the plasmid pVSVFL(+) that gives rise to infectious VSV. The locations of the VSV genes encoding the five proteins N, P, M, G, and L are shown. The stippled region from Sac I to Xho I represents the pBSSK⁺ vector sequence, and the hatched segments represent the regions of the VSV genome generated by
20 PCR. Transcription from the T7 promoter generates the complete (+) strand VSV RNA.

Figure 5. Proteins present in wild-type and recombinant VSVs. Proteins from 1% of the virus recovered from approximately 5×10^6 infected BHK cells were separated
25 by SDS-PAGE (10% acrylamide) and visualized by staining with Coomassie brilliant blue. Positions of the five VSV proteins are indicated.

Figure 6. Identification of a restriction enzyme recognition sequence in the recombinant VSV. A 620
30 nucleotide segment of genomic RNA isolated from wildtype and recombinant VSV was amplified by reverse transcription and PCR using the primers 5'-CATTCAAGACGCTGCTTCGCAACTCC (SEQ ID NO:32) and 5'-CATGAATGTTAACATCTCAAGA (SEQ ID NO:33). Controls in which reverse transcriptase was omitted from the
35 reaction are indicated. DNA samples were either digested with Nhe I or left undigested prior to electrophoresis on a 6% polyacrylamide gel as indicated. DNA was detected by

staining with ethidium bromide. Sizes of DNA markers are indicated on the left.

Figure 7. Autoradiogram showing the sequence of genomic RNA from recombinant VSV. RNA prepared from recombinant VSV was sequenced by the dideoxy method using reverse transcriptase. The written sequence corresponds to nucleotides 1563-1593 in the G mRNA (Rose and Gallione, 1981, J. Virol. 39:519-528). The underlined sequence represents the four nucleotides that were changed to generate the Nhe I site.

Figure 8. Protein analysis of recombinant VSV expressing the glycoprotein from the New Jersey serotype. Proteins from 1% of the virus pelleted from the medium of approximately 5×10^6 BHK cells infected for 24 hours with wildtype VSV₁ (lane 1), recombinant VSV_{INDG} (lane 2) or wildtype VSV_N (lane 3) were separated by SDS-PAGE (10% acrylamide). The proteins were visualized by staining with Coomassie brilliant blue. Positions of viral proteins are indicated.

5. DETAILED DESCRIPTION OF THE INVENTION

The present invention provides recombinant replicable vesiculoviruses. The prior art has unsuccessfully attempted to produce replicable vesiculoviruses from cloned DNA. In contrast, the invention provides a method which, for the first time, has successfully allowed the production and recovery of replicable vesiculoviruses, as well as recombinant replicable vesiculoviruses, from cloned DNA. Expression of the full-length positive-strand vesiculovirus RNA in host cells has successfully allowed the generation of recombinant vesiculoviruses from DNA, providing recombinant viruses that do not cause serious pathology in humans and that can be obtained in high titers, that have use as vaccines.

The vesiculoviruses of the invention are produced by providing in an appropriate host cell: (a) DNA that can be transcribed to yield (encodes) vesiculovirus antigenomic (+) RNA (complementary to the vesiculovirus genome), (b) a

recombinant source of vesiculovirus N protein, (c) a recombinant source of vesiculovirus P protein, and (d) a recombinant source of vesiculovirus L protein; under conditions such that the DNA is transcribed to produce the
5 antigenomic RNA, and a vesiculovirus is produced that contains genomic RNA complementary to the antigenomic RNA produced from the DNA.

The invention provides an infectious recombinant vesiculovirus capable of replication in an animal into which
10 the recombinant vesiculovirus is introduced, in which the genome of the vesiculovirus comprises foreign RNA which is not naturally a part of the vesiculovirus genome. The recombinant vesiculovirus is formed by producing vesiculoviruses according to the method of the invention, in
15 which regions of the DNA encoding vesiculovirus antigenomic (+) RNA that are nonessential for viral replication have been inserted into or replaced with foreign DNA.

Since the viruses are replicable (i.e., not replication-defective), they encode all the vesiculovirus
20 machinery necessary for replication in a cell upon infection by the virus.

In a preferred embodiment, the recombinant vesiculovirus is a recombinant vesicular stomatitis virus (VSV).

25 In another preferred embodiment, the foreign RNA contained within the genome of the recombinant vesiculovirus (originally encoded by the foreign DNA), upon expression in an appropriate host cell, produces a protein or peptide that is antigenic or immunogenic. Such an antigenic or
30 immunogenic protein or peptide whose expression is directed by the foreign RNA (present in the negative sense) within the vesiculovirus genome (by expression from the (+) antigenomic message) shall be referred to hereinafter as the "Antigen." Appropriate Antigens include but are not limited to known
35 antigens of pathogenic microorganisms or of tumors, as well as fragments or derivatives of such antigens displaying the antigenicity or immunogenicity of such antigens. A protein

displays the antigenicity of an antigen when the protein is capable of being immunospecifically bound by an antibody to the antigen. A protein displays the immunogenicity of an antigen when it elicits an immune response to the antigen (e.g., when immunization with the protein elicits production of an antibody that immunospecifically binds the antigen or elicits a cell-mediated immune response directed against the antigen).

The recombinant vesiculoviruses of the invention have use as vaccines. In one embodiment, where the foreign RNA directs production of an Antigen (originally encoded by the foreign DNA used to produce the recombinant vesiculovirus or its predecessor) that induces an immune response against a pathogen, the vaccines of the invention have use in the treatment or prevention of infections by such a pathogen (particularly a pathogenic microorganism), and its clinical manifestations, i.e., infectious disease. The invention thus provides methods of prevention or treatment of infection and infectious disease comprising administering to a subject in which such treatment or prevention is desired one or more of the recombinant vesiculoviruses of the invention. The recombinant vesiculoviruses also have uses in diagnosis, and monitoring progression of infectious disorders, including response to vaccination and/or therapy.

In another embodiment, where the Antigen induces an immune response against a tumor, the recombinant viruses of the invention have uses in cancer immunoprophylaxis, immunotherapy, and diagnosis, and monitoring of tumor progression or regression.

The recombinant vesiculoviruses can be used as live vaccines, or can be inactivated for use as killed vaccines. The recombinant viruses can also be used to produce large quantities of readily purified antigen, e.g., for use in subunit vaccines.

In a specific embodiment, the foreign DNA used initially for production of the recombinant vesiculoviruses can also comprise a sequence encoding a detectable marker,

e.g., β -galactosidase, β -glucuronidase, β -geo (Friedrich & Soriano, 1991, Genes Dev. 5:1513-1523).

In another specific embodiment, the foreign DNA can also comprise a sequence encoding a cytokine capable of
5 stimulating an immune response. Such cytokines include but are not limited to, interleukin-2, interleukin-6, interleukin-12, interferons, and granulocyte-macrophage colony stimulating factors.

In a preferred aspect, upon infection with a
10 recombinant vesiculovirus of the invention, the Antigen is expressed as a nonfusion protein. In a less preferred embodiment, the Antigen is expressed as a fusion protein, e.g., to the viral G protein. "Fusion protein," as used herein, refers to a protein comprising an amino acid sequence
15 from a first protein covalently linked via a peptide bond at its carboxy terminus to the amino terminus of an amino acid sequence from a second, different protein.

In one embodiment, a vaccine formulation of the invention contains a single type of recombinant vesiculovirus
20 of the invention. In another embodiment, a vaccine formulation comprises a mixture of two or more recombinant viruses of the invention.

The vaccine formulations of the invention provide one or more of the following benefits: stability for long
25 periods without refrigeration; ease of production; low cost and high titer of production; ability to be administered by local workers without advanced medical training; and involving administration of a microorganism that is known not to cause serious disease in humans.

30 The present invention also provides a host cell infected with a recombinant vesiculovirus capable of replication. In one embodiment, the host cell is a mammalian cell. Preferably, the mammalian cell is a hamster kidney cell.

35

5.1. DNA THAT CAN BE TRANSCRIBED TO PRODUCE
VESICULOVIRUS ANTIGENOMIC (+) RNA

Many vesiculoviruses are known in the art and can be made recombinant according to the methods of the invention. Examples of such vesiculoviruses are listed in Table I.

TABLE I

MEMBERS OF THE VESICULOVIRUS GENUS

	<u>Virus</u>	<u>Source of virus in nature</u>
	VSV-New Jersey	Mammals, mosquitoes, midges, blackflies, houseflies
	VSV-Indiana	Mammals, mosquitoes, sandflies
15	Alagoas	Mammals, sandflies
	Cocal	Mammals, mosquitoes, mites
	Jurona	Mosquitoes
	Carajas	Sandflies
20	Maraba	Sandflies
	Piry	Mammals
	Calchaqui	Mosquitoes
25	Yug Bogdanovac	Sandflies
	Isfahan	Sandflies, ticks
	Chandipura	Mammals, sandflies
	Perinct	Mosquitoes, sandflies
30	Porton-S	Mosquitoes

Any DNA that can be transcribed to produce vesiculovirus antigenomic (+) RNA (complementary to the VSV genome) can be used for the construction of a recombinant DNA containing foreign DNA encoding an Antigen, for use in

producing the recombinant vesiculoviruses of the invention. DNA that can be transcribed to produce vesiculovirus antigenomic (+) RNA (such DNA being referred to herein as "vesiculovirus (-) DNA") is available in the art and/or can
5 be obtained by standard methods. In particular, plasmid pVSVFL(+), containing VSV (-) DNA that is preferred for use in the present invention, has been deposited with the ATCC and assigned accession no. 97134. In a preferred aspect, DNA that can be transcribed to produce VSV (+) RNA, [i.e.,
10 VSV (-) DNA], is used. VSV (-) DNA for any serotype or strain known in the art, e.g., the New Jersey or Indiana serotypes of VSV, can be used. The complete nucleotide and deduced protein sequence of the VSV genome is known, and is available as Genbank VSVCG, Accession No. J02428; NCBI Seq ID
15 335873; and is published in Rose and Schubert, 1987, in *The Viruses: The Rhabdoviruses*, Plenum Press, NY, pp. 129-166. Partial sequences of other vesiculovirus genomes have been published and are available in the art. The complete
sequence of the VSV (-) DNA that is used in a preferred
20 embodiment is contained in plasmid pVSVFL(+) and is shown in Figure 1; also shown are with the predicted sequences of the VSV proteins (this sequence contains several sequence corrections relative to that obtainable from Genbank). Vesiculovirus (-) DNA, if not already available, can be
25 prepared by standard methods, as follows: If vesiculoviral cDNA is not already available, vesiculovirus genomic RNA can be purified from virus preparations, and reverse transcription with long distance polymerase chain reaction used to generate the vesiculovirus (-) DNA. Alternatively,
30 after purification of genomic RNA, VSV mRNA can be synthesized *in vitro*, and cDNA prepared by standard methods, followed by insertion into cloning vectors (see, e.g., Rose and Gallione, 1981, *J. Virol.* 39(2):519-528). Individual cDNA clones of vesiculovirus RNA can be joined by use of
35 small DNA fragments covering the gene junctions, generated by use of reverse transcription and polymerase chain reaction (RT-PCR) (Mullis and Faloona, 1987, *Meth. Enzymol.*

155:335-350) from VSV genomic RNA (see Section 6, *infra*).
Vesiculoviruses are available in the art. For example, VSV
can be obtained from the American Type Culture Collection.

In a preferred embodiment, one or more, preferably
5 unique, restriction sites (e.g., in a polylinker) are
introduced into the vesiculovirus (-) DNA, in intergenic
regions, or 5' of the sequence complementary to the 3' end of
the vesiculovirus genome, or 3' of the sequence complementary
to the 5' end of the vesiculovirus genome, to facilitate
10 insertion of the foreign DNA.

In a preferred method of the invention, the
vesiculovirus (-) DNA is constructed so as to have a promoter
operatively linked thereto. The promoter should be capable
of initiating transcription of the (-) DNA in an animal or
15 insect cell in which it is desired to produce the recombinant
vesiculovirus. Promoters which may be used include, but are
not limited to, the SV40 early promoter region (Bernoist and
Chambon, 1981, Nature 290:304-310), the promoter contained in
the 3' long terminal repeat of Rous sarcoma virus (Yamamoto,
20 et al., 1980, Cell 22:787-797), the herpes thymidine kinase
promoter (Wagner et al., 1981, Proc. Natl. Acad. Sci. U.S.A.
78:1441-1445), the regulatory sequences of the
metallothionein gene (Brinster et al., 1982, Nature
296:39-42); heat shock promoters (e.g., hsp70 for use in
25 *Drosophila* S2 cells); the ADC (alcohol dehydrogenase)
promoter, PGK (phosphoglycerol kinase) promoter, alkaline
phosphatase promoter, and the following animal
transcriptional control regions, which exhibit tissue
specificity and have been utilized in transgenic animals:
30 elastase I gene control region which is active in pancreatic
acinar cells (Swift et al., 1984, Cell 38:639-646; Ornitz et
al., 1986, Cold Spring Harbor Symp. Quant. Biol. 50:399-409;
MacDonald, 1987, Hepatology 7:425-515); insulin gene control
region which is active in pancreatic beta cells (Hanahan,
35 1985, Nature 315:115-122), immunoglobulin gene control region
which is active in lymphoid cells (Grosschedl et al., 1984,
Cell 38:647-658; Adames et al., 1985, Nature 318:533-538;

Alexander et al., 1987, Mol. Cell. Biol. 7:1436-1444), mouse mammary tumor virus control region which is active in testicular, breast, lymphoid and mast cells (Leder et al., 1986, Cell 45:485-495), albumin gene control region which is
5 active in liver (Pinkert et al., 1987, Genes and Devel. 1:268-276), alpha-fetoprotein gene control region which is active in liver (Krumlauf et al., 1985, Mol. Cell. Biol. 5:1639-1648; Hammer et al., 1987, Science 235:53-58; alpha 1-antitrypsin gene control region which is active in the liver
10 (Kelsey et al., 1987, Genes and Devel. 1:161-171), beta-globin gene control region which is active in myeloid cells (Mogram et al., 1985, Nature 315:338-340; Kollias et al., 1986, Cell 46:89-94; myelin basic protein gene control region which is active in oligodendrocyte cells in the brain
15 (Readhead et al., 1987, Cell 48:703-712); and myosin light chain-2 gene control region which is active in skeletal muscle (Sani, 1985, Nature 314:283-286). Preferably, the promoter is an RNA polymerase promoter, preferably a bacteriophage or viral or insect RNA polymerase promoter,
20 including but not limited to the promoters for T7 RNA polymerase, SP6 RNA polymerase, and T3 RNA polymerase. If an RNA polymerase promoter is used in which the RNA polymerase is not endogenously produced by the host cell in which it is desired to produce the recombinant vesiculovirus, a
25 recombinant source of the RNA polymerase must also be provided in the host cell.

The vesiculovirus (-) DNA can be operably linked to a promoter before or after insertion of foreign DNA encoding an Antigen. Preferably, a transcriptional terminator is
30 situated downstream of the vesiculovirus (-) DNA.

In another preferred embodiment, a DNA sequence that can be transcribed to produce a ribozyme sequence is situated at the immediate 3' end of the vesiculovirus (-) DNA, prior to the transcriptional termination signal, so that
35 upon transcription a self-cleaving ribozyme sequence is produced at the 3' end of the antigenomic RNA, which ribozyme sequence will autolytically cleave (after a U) this fusion

transcript to release the exact 3' end of the vesiculovirus antigenomic (+) RNA. Any ribozyme sequence known in the art may be used, as long as the correct sequence is recognized and cleaved. (It is noted that hammerhead ribozyme is probably not suitable for use.) In a preferred aspect, hepatitis delta virus (HDV) ribozyme is used (Perrotta and Been, 1991, Nature 350:434-436; Pattnaik et al., 1992, Cell 69:1011-1020).

A preferred VSV(-) DNA for use, for insertion of foreign DNA, is that shown in Fig. 1 and contained in plasmid pVSVFL(+), in which a T7 RNA polymerase promoter is present 5' of the sequence complementary to the 3' end of the VSV genome. Plasmid pVSVFL(+) thus comprises (in 5' to 3' order) the following operably linked components: the T7 RNA polymerase promoter, VSV (-) DNA, a DNA sequence that is transcribed to produce an HDV ribozyme sequence (immediately downstream of the VSV (-) DNA), and a T7 RNA polymerase transcription termination site. A plasmid that can also be made and used is plasmid pVSVSS1, a portion of the sequence of which is shown in Fig. 2, in which a synthetic DNA polylinker, facilitating insertion of foreign DNA, has been inserted into pVSVFL(+) between the G and L coding regions. The polylinker was synthesized on a DNA synthesizer so as to have ends compatible for ligation into an NheI site, and to contain the unique restriction enzyme recognition sites XmaI, SmaI, and NotI, facilitating insertion of foreign DNA generated by cleavage with one of these enzymes or ligated to a linker containing a recognition site for one of these enzymes (which is then subjected to cleavage prior to insertion).

The foreign DNA encoding an Antigen is inserted into any region, or replaces any region, of the vesiculovirus (-) DNA that is not essential for vesiculovirus replication. In a preferred embodiment, the foreign DNA is thus inserted into an intergenic region, or a portion of the vesiculovirus (-) DNA that is transcribed to form the noncoding region of a viral mRNA. In a preferred embodiment,

the invention provides a nucleic acid comprising the DNA sequence of plasmid pVSVFL(+) as depicted in Figure 1 from nucleotide numbers 623-12088 (a portion of SEQ ID NO:1), in which a region nonessential for vesiculovirus replication has been inserted into or replaced by foreign DNA.

Vesiculoviruses have a defined intergenic structure. Extensive homologies are found around the intergenic dinucleotides (Fig. 3). These regions have the common structure (3')AUACUUUUUUUNAUGUCNNUAG(5') (SEQ ID NO:34), in which N indicates any nucleotide (thus three variable positions are present) and the intergenic dinucleotide is underlined. These dinucleotide spacers are GA, except at the NS-M junction, where the dinucleotide is CA. The first 11 nucleotides of the common sequence are complementary to the sequence (5') . . . UAUGAAAAAA . . . (3') (SEQ ID NO:35) that occurs at the mRNA-polyadenylate[poly(A)] junction in each mRNA including L. Reiterative copying of the U residues by the VSV polymerase presumably generates the poly(A) tail on each mRNA (McGeoch, 1979, Cell 17:3199; Rose, 1980, Cell 19:415; Schubert et al., 1980, J. Virol. 34:550). The sequence complementary to the 5' end of the mRNA follows the intergenic dinucleotide. The L mRNA also terminates with the sequence UAUG-poly(A) encoded by the sequence (3')AUACUUUUUU (SEQ ID NO:36) and is presumably also polyadenylated by a polymerase "slippage" mechanism (Schubert et al., 1980, J. Virol. 34:550; Schubert and Lazarini, 1981, J. Virol. 38:256).

Thus, intergenic regions in vesiculovirus (-) DNA consist of three parts, triggering transcriptional termination and reinitiation present both 5' and 3' to each gene (presented as the 5' to 3' sequence of the positive sense strand of vesiculovirus (-) DNA): (a) TATGAAAAAA (SEQ ID NO:37), followed by (b) the dinucleotide GT or CT, followed by (c) AACAG. Therefore, in a preferred aspect, foreign DNA encoding an Antigen can readily be expressed as a nonfusion protein from intergenic regions, simply by ensuring

that this three-part intergenic region is reconstituted -- i.e., that this intergenic region appears 5' and 3' to the foreign DNA and also 5' and 3' to the adjacent genes. For example, in a preferred embodiment, DNA consisting of (a) this three-part intergenic region, fused to (b) foreign DNA coding for a desired Antigen (preferably including the Antigen gene's native start and stop codons for initiation), is inserted into a portion of the vesiculovirus (-) DNA that is transcribed to form the 3' noncoding region of any vesiculovirus mRNA. In a particularly preferred aspect, the foreign DNA is inserted in the noncoding region between G and L.

In an alternative embodiment, the foreign DNA can be inserted into the G gene, so as to encode a fusion protein with G, for resultant surface display of the Antigen on the vesiculovirus particle. Selection should be undertaken to ensure that the foreign DNA insertion does not disrupt G protein function.

In a preferred embodiment, an Antigen expressed by a recombinant vesiculovirus is all or a portion of an envelope glycoprotein of a virus other than a vesiculovirus. Such an Antigen can replace the endogenous vesiculovirus G protein in the vesiculovirus, or can be expressed as a fusion with the endogenous G protein, or can be expressed in addition to the endogenous G protein either as a fusion or nonfusion protein. In a specific embodiment, such an Antigen forms a part of the vesiculovirus envelope and thus is surface-displayed in the vesiculovirus particle. By way of example, gp160 or a fragment thereof of Human Immunodeficiency Virus can be the Antigen, which is cleaved to produce gp120 and gp41 (see Owens and Rose, 1993, J. Virol. 67(1):360-365). In a specific embodiment, the G gene of VSV in the VSV (-) DNA of plasmid pVSVFL(+) can be easily excised and replaced, by cleavage at the NheI and MluI sites flanking the G gene and insertion of the desired sequence. In another specific embodiment, the Antigen is a foreign

envelope glycoprotein or portion thereof that is expressed as a fusion protein comprising the cytoplasmic domain (and, optionally, also the transmembrane region) of the native vesiculovirus G protein (see Owens and Rose, 1993, J. Virol. 5 67(1):360-365). Such a fusion protein can replace or be expressed in addition to the endogenous vesiculovirus G protein. As shown by way of example in Section 6 below, the entire native G coding sequence can be replaced by a coding sequence of a different G to produce recombinant replicable 10 vesiculoviruses that express a non-native glycoprotein. While recombinant vesiculoviruses that express and display epitope(s) of envelope glycoproteins of other viruses can be used as live vaccines, such vesiculoviruses also are particularly useful as killed vaccines, as well as in the 15 production of subunit vaccines containing the vesiculovirus-produced protein comprising such epitope(s).

In a specific embodiment, a recombinant vesiculovirus of the invention expresses in a host to which it is administered one or more Antigens. In one embodiment, 20 a multiplicity of Antigens are expressed, each displaying different antigenicity or immunogenicity.

5.2. DNA SEQUENCES ENCODING ANTIGENS

The invention provides recombinant vesiculoviruses 25 capable of replication that have a foreign RNA sequence inserted into or replacing a site of the genome nonessential for replication, wherein the foreign RNA sequence (which is in the negative sense) directs the production of an Antigen capable of being expressed in a host infected by the 30 recombinant virus. This recombinant genome is originally produced by insertion of foreign DNA encoding the Antigen into the vesiculovirus (-) DNA. Any DNA sequence which encodes an immunogenic (capable of provoking an immune response) Antigen, which produces prophylactic or therapeutic 35 immunity against a disease or disorder, when expressed as a fusion or, preferably, nonfusion protein in a recombinant vesiculovirus of the invention, alone or in combination with

other Antigens expressed by the same or a different vesiculovirus recombinant, can be isolated for use in the vaccine formulations of the present invention.

In a preferred embodiment, expression of an Antigen
5 by a recombinant vesiculovirus induces an immune response against a pathogenic microorganism. For example, an Antigen may display the immunogenicity or antigenicity of an antigen found on bacteria, parasites, viruses, or fungi which are causative agents of diseases or disorders. In a preferred
10 embodiment, Antigens displaying the antigenicity or immunogenicity of antigens of animal viruses of veterinary importance (for example, which cause diseases or disorders in non-human animals such as domestic or farm animals, e.g., cows, chickens, horses, dogs, cats, etc.) are used. In
15 another embodiment, Antigens displaying the antigenicity or immunogenicity of an antigen of a human pathogen are used.

To determine immunogenicity or antigenicity by detecting binding to antibody, various immunoassays known in the art can be used, including but not limited to competitive
20 and non-competitive assay systems using techniques such as radioimmunoassays, ELISA (enzyme linked immunosorbent assay), "sandwich" immunoassays, immunoradiometric assays, gel diffusion precipitin reactions, immunodiffusion assays, in situ immunoassays (using colloidal gold, enzyme or
25 radioisotope labels, for example), western blots, immunoprecipitation reactions, agglutination assays (e.g., gel agglutination assays, hemagglutination assays), complement fixation assays, immunofluorescence assays, protein A assays, and immunoelectrophoresis assays, etc. In
30 one embodiment, antibody binding is detected by detecting a label on the primary antibody. In another embodiment, the primary antibody is detected by detecting binding of a secondary antibody or reagent to the primary antibody. In a further embodiment, the secondary antibody is labelled. Many
35 means are known in the art for detecting binding in an immunoassay and are envisioned for use. In one embodiment for detecting immunogenicity, T cell-mediated responses can

be assayed by standard methods, e.g., in vitro cytotoxicity assays or in vivo delayed-type hypersensitivity assays.

Parasites and bacteria expressing epitopes (antigenic determinants) that can be expressed by recombinant vesiculoviruses (wherein the foreign RNA directs the production of an antigen of the parasite or bacteria or a derivative thereof containing an epitope thereof) include but are not limited to those listed in Table II.

10

TABLE II

PARASITES AND BACTERIA EXPRESSING EPITOPES
THAT CAN BE EXPRESSED BY RECOMBINANT VESICULOVIRUSES

15

PARASITES:

Plasmodium spp.
Eimeria spp.

BACTERIA:

20

Vibrio cholerae
Streptococcus pneumoniae
Neisseria meningitidis
Neisseria gonorrhoeae
Corynebacterium diphtheriae
Clostridium tetani
Bordetella pertussis
Haemophilus spp. (e.g., *influenzae*)
Chlamydia spp.
Enterotoxigenic *Escherichia coli*

25

In another embodiment, the Antigen comprises an epitope of an antigen of a nematode, to protect against disorders caused by such worms.

30

In another specific embodiment, any DNA sequence which encodes a *Plasmodium* epitope, which when expressed by a recombinant vesiculovirus, is immunogenic in a vertebrate host, can be isolated for insertion into vesiculovirus (-) DNA according to the present invention. The species of *Plasmodium* which can serve as DNA sources include but are not limited to the human malaria parasites *P. falciparum*, *P.*

35

malariae, *P. ovale*, *P. vivax*, and the animal malaria parasites *P. berghei*, *P. yoelii*, *P. knowlesi*, and *P. cynomolgi*. In a particular embodiment, the epitope to be expressed is an epitope of the circumsporozoite (CS) protein of a species of *Plasmodium* (Miller et al., 1986, Science 234:1349).

In yet another embodiment, the Antigen comprises a peptide of the β subunit of Cholera toxin (Jacob et al., 1983, Proc. Natl. Acad. Sci. USA 80:7611).

10 Viruses expressing epitopes (antigenic determinants) that can be expressed by recombinant vesiculoviruses (wherein the foreign RNA directs the production of an antigen of the virus or a derivative thereof comprising an epitope thereof) include but are not limited to
15 those listed in Table III, which lists such viruses by family for purposes of convenience and not limitation (see 1990, Fields Virology, 2d ed., Fields and Knipe (eds.), Raven Press, NY).

20

TABLE III

VIRUSES EXPRESSING EPITOPES THAT CAN
BE EXPRESSED BY RECOMBINANT VESICULOVIRUSES

- | | |
|----|--|
| 25 | I. Picornaviridae |
| | Enteroviruses |
| | Poliovirus |
| | Coxsackievirus |
| | Echovirus |
| | Rhinoviruses |
| | Hepatitis A Virus |
| 30 | II. Caliciviridae |
| | Norwalk group of viruses |
| | III. Togaviridae and Flaviviridae |
| | Togaviruses (e.g., Dengue virus) |
| | Alphaviruses |
| | Flaviviruses (e.g., Hepatitis C virus) |
| | Rubella virus |
| 35 | IV. Coronaviridae |
| | Coronaviruses |

- V. Rhabdoviridae
Rabies virus
- VI. Filoviridae
Marburg viruses
Ebola viruses
- 5 VII. Paramyxoviridae
Parainfluenza virus
Mumps virus
Measles virus
Respiratory syncytial virus
- 10 VIII. Orthomyxoviridae
Orthomyxoviruses (e.g., Influenza virus)
- IX. Bunyaviridae
Bunyaviruses
- X. Arenaviridae
Arenaviruses
- 15 XI. Reoviridae
Reoviruses
Rotaviruses
Orbiviruses
- XII. Retroviridae
20 Human T Cell Leukemia Virus type I
Human T Cell Leukemia Virus type II
Human Immunodeficiency Viruses (e.g.,
type I and type II)
Simian Immunodeficiency Virus
Lentiviruses
- XIII. Papoviridae
25 Polyomaviruses
Papillomaviruses
Adenoviruses
- XIV. Parvoviridae
Parvoviruses
- 30 XV. Herpesviridae
Herpes Simplex Viruses
Epstein-Barr virus
Cytomegalovirus
Varicella-Zoster virus
Human Herpesvirus-6
Cercopithecine Herpes Virus 1 (B virus)
- 35 XVI. Poxviridae
Poxviruses

XVIII. Hepadnaviridae
Hepatitis B virus

5 In specific embodiments, the Antigen encoded by the
foreign sequences that is expressed upon infection of a host
by the recombinant vesiculovirus, displays the antigenicity
or immunogenicity of an influenza virus hemagglutinin
(Genbank accession no. JO2132; Air, 1981, Proc. Natl. Acad.
10 Sci. USA 78:7639-7643; Newton et al., 1983, Virology
128:495-501); human respiratory syncytial virus G
glycoprotein (Genbank accession no. Z33429; Garcia et al.,
1994, J. Virol.; Collins et al., 1984, Proc. Natl. Acad.
Sci. USA 81:7683); core protein, matrix protein or other
15 protein of Dengue virus (Genbank accession no. M19197; Hahn
et al., 1988, Virology 162:167-180), measles virus
hemagglutinin (Genbank accession no. M81899; Rota et al.,
1992, Virology 188:135-142); and herpes simplex virus type 2
glycoprotein gB (Genbank accession no. M14923; Bzik et al.,
20 1986, Virology 155:322-333).

In another embodiment, one or more epitopes of the
fusion protein of respiratory syncytial virus (RSV) can be
expressed as an Antigen.

Other Antigens that can be expressed by a
25 recombinant vesiculovirus include but are not limited to
those displaying the antigenicity or immunogenicity of the
following antigens: Poliovirus I VP1 (Emini et al., 1983,
Nature 304:699); envelope glycoproteins of HIV I (Putney et
al., 1986, Science 234:1392-1395); Hepatitis B surface
30 antigen (Itoh et al., 1986, Nature 308:19; Neurath et al.,
1986, Vaccine 4:34); Diphtheria toxin (Audibert et al., 1981,
Nature 289:543); streptococcus 24M epitope (Beachey, 1985,
Adv. Exp. Med. Biol. 185:193); and gonococcal pilin (Rothbard
and Schoolnik, 1985, Adv. Exp. Med. Biol. 185:247).

35 In other embodiments, the Antigen expressed by the
recombinant vesiculovirus displays the antigenicity or

immunogenicity of pseudorabies virus g50 (gpD), pseudorabies virus II (gpB), pseudorabies virus gIII (gpC), pseudorabies virus glycoprotein H, pseudorabies virus glycoprotein E, transmissible gastroenteritis glycoprotein 195, transmissible
 5 gastroenteritis matrix protein, swine rotavirus glycoprotein 38, swine parvovirus capsid protein, *Serpulina* *hyodysenteriae* protective antigen, Bovine Viral Diarrhea glycoprotein 55, Newcastle Disease Virus hemagglutinin-neuraminidase, swine flu hemagglutinin, or swine flu
 10 neuraminidase.

In various embodiments, the Antigen expressed by the recombinant vesiculovirus displays the antigenicity or immunogenicity of an antigen derived from *Serpulina* *hyodysenteriae*, Foot and Mouth Disease Virus, Hog Colera
 15 Virus, swine influenza virus, African Swine Fever Virus, *Mycoplasma hyopneumoniae*, infectious bovine rhinotracheitis virus (e.g., infectious bovine rhinotracheitis virus glycoprotein E or glycoprotein G), or infectious
 20 laryngotracheitis virus (e.g., infectious laryngotracheitis virus glycoprotein G or glycoprotein I).

In another embodiment, the Antigen displays the antigenicity or immunogenicity of a glycoprotein of La Crosse Virus (Gonzales-Scarano et al., 1982, Virology 120:42), Neonatal Calf Diarrhea Virus (Matsuno and Inouye, 1983,
 25 Infection and Immunity 39:155), Venezuelan Equine Encephalomyelitis Virus (Mathews and Roehrig, 1982, J. Immunol. 129:2763), Punta Toro Virus (Dalrymple et al., 1981, in Replication of Negative Strand Viruses, Bishop and Compans (eds.), Elsevier, NY, p. 167), Murine Leukemia Virus (Steeves
 30 et al., 1974, J. Virol. 14:187), or Mouse Mammary Tumor Virus (Massey and Schochetman, 1981, Virology 115:20).

In another embodiment, the Antigen displays the antigenicity or immunogenicity of an antigen of a human pathogen, including but not limited to human herpesvirus,
 35 herpes simplex virus-1, herpes simplex virus-2, human cytomegalovirus, Epstein-Barr virus, Varicella-Zoster virus, human herpesvirus-6, human herpesvirus-7, human influenza

virus, human immunodeficiency virus, rabies virus, measles virus, hepatitis B virus, hepatitis C virus, *Plasmodium falciparum*, and *Bordetella pertussis*.

In a specific embodiment of the invention, a
5 recombinant vesiculovirus expresses hepatitis B virus core protein and/or hepatitis B virus surface antigen or a fragment or derivative thereof (see, e.g., U.K. Patent Publication No. GB 2034323A published June 4, 1980; Ganem and Varmus, 1987, Ann. Rev. Biochem. 56:651-693; Tiollais et al.,
10 1985, Nature 317:489-495). The HBV genome (subtype adw) is contained in plasmid pAM6 (Moriarty et al., 1981, Proc. Natl. Acad. Sci. USA 78:2606-2610, available from the American Type Culture Collection (ATCC), Accession No. 45020), a pBR322-based vector that is replicable in *E. coli*.

15 In another embodiment, the Antigen expressed by the recombinant vesiculovirus displays the antigenicity or immunogenicity of an antigen of equine influenza virus or equine herpesvirus. Examples of such antigens are equine influenza virus type A/Alaska 91 neuraminidase, equine
20 influenza virus type A/Miami 63 neuraminidase, equine influenza virus type A/Kentucky 81 neuraminidase equine herpesvirus type 1 glycoprotein B, and equine herpesvirus type 1 glycoprotein D.

In another embodiment, the Antigen displays the
25 antigenicity or immunogenicity of an antigen of bovine respiratory syncytial virus or bovine parainfluenza virus. For example, such antigens include but are not limited to bovine respiratory syncytial virus attachment protein (BRSV G), bovine respiratory syncytial virus fusion protein
30 (BRSV F), bovine respiratory syncytial virus nucleocapsid protein (BRSV N), bovine parainfluenza virus type 3 fusion protein, and the bovine parainfluenza virus type 3 hemagglutinin neuraminidase.

In another embodiment, the Antigen displays the
35 antigenicity or immunogenicity of bovine viral diarrhea virus glycoprotein 48 or glycoprotein 53.

In another embodiment, the Antigen displays the antigenicity or immunogenicity of an antigen of infectious bursal disease virus. Examples of such antigens are infectious bursal disease virus polyprotein and VP2.

- 5 Potentially useful antigens or derivatives thereof for use as Antigens expressed by recombinant vesiculoviruses can be identified by various criteria, such as the antigen's involvement in neutralization of a pathogen's infectivity (Norrby, 1985, Summary, *in* Vaccines85, Lerner et al. (eds.),
10 Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, pp. 388-389), type or group specificity, recognition by patients' antisera or immune cells, and/or the demonstration of protective effects of antisera or immune cells specific for the antigen. In addition, the antigen's encoded epitope
15 should preferably display a small or no degree of antigenic variation in time or amongst different isolates of the same pathogen.

- In a preferred embodiment, the foreign DNA inserted into the vesiculovirus (-) DNA encodes an immunopotent
20 dominant epitope of a pathogen. Foreign DNA encoding epitopes which are reactive with antibody although incapable of eliciting immune responses, still have potential uses in immunoassays (see Section 5.8, *infra*).

- In another embodiment, foreign RNA of the
25 recombinant vesiculovirus directs the production of an Antigen comprising an epitope, which when the recombinant vesiculovirus is introduced into a desired host, induces an immune response that protects against a condition or disorder caused by an entity containing the epitope. For example, the
30 Antigen can be a tumor specific antigen or tumor-associated antigen, for induction of a protective immune response against a tumor (e.g., a malignant tumor). Such tumor-specific or tumor-associated antigens include but are not limited to KS 1/4 pan-carcinoma antigen (Perez and Walker,
35 1990, J. Immunol. 142:3662-3667; Bumal, 1988, Hybridoma 7(4):407-415); ovarian carcinoma antigen (CA125) (Yu et al., 1991, Cancer Res. 51(2):468-475); prostatic acid phosphate

(Tailor et al., 1990, Nucl. Acids Res. 18(16):4928); prostate specific antigen (Henttu and Vihko, 1989, Biochem. Biophys. Res. Comm. 160(2):903-910; Israeli et al., 1993, Cancer Res. 53:227-230; melanoma-associated antigen p97 (Estin et al., 5 1989, J. Natl. Cancer Instit. 81(6):445-446); melanoma antigen gp75 (Vijayasardahl et al., 1990, J. Exp. Med. 171(4):1375-1380); high molecular weight melanoma antigen (Natali et al., 1987, Cancer 59:55-63); and prostate specific membrane antigen.

10 In another embodiment of the invention, the Antigen expressed by the recombinant vesiculovirus comprises large regions of proteins which contain several B cell epitopes (i.e., epitopes capable of enticing a humoral immune response) and T cell epitopes (i.e., epitopes capable of 15 inducing a cell-mediated immune response).

Peptides or proteins which are known to contain antigenic determinants can be used as the Antigen. If specific desired antigens are unknown, identification and characterization of immunoreactive sequences can be carried 20 out. One way in which to accomplish this is through the use of monoclonal antibodies generated to the surface or other molecules of a pathogen or tumor, as the case may be. The peptide sequences capable of being recognized by the antibodies are defined epitopes. Alternatively, small 25 synthetic peptides conjugated to carrier molecules can be tested for generation of monoclonal antibodies that bind to the sites corresponding to the peptide, on the intact molecule (see, e.g., Wilson et al., 1984, Cell 37:767).

In a specific embodiment, appropriate Antigens, 30 including fragments or derivatives of known antigens, can be identified by virtue of their hydrophilicity, by carrying out a hydrophilicity analysis (Hopp and Woods, 1981, Proc. Natl. Acad. Sci. USA 78:3824) to generate a hydrophilicity profile. A hydrophilicity profile can be used to identify the 35 hydrophobic and hydrophilic regions of a protein and the corresponding regions of the gene sequence which encode such proteins. Hydrophilic regions are predicted to be

immunogenic/antigenic. Other methods known in the art which may be employed for the identification and characterization of antigenic determinants are also within the scope of the invention.

5 The foreign DNA encoding the Antigen, that is inserted into a non-essential site of the vesiculovirus (-) DNA, optionally can further comprise a foreign DNA sequence encoding a cytokine capable of being expressed and stimulating an immune response in a host infected by the
10 recombinant vesiculovirus. For example, such cytokines include but are not limited to interleukin-2, interleukin-6, interleukin-12, interferons, granulocyte-macrophage colony stimulating factors, and interleukin receptors.

 The foreign DNA optionally can further comprise a
15 sequence encoding and capable of expressing a detectable marker (e.g., β galactosidase).

5.3. CONSTRUCTION OF VESICULOVIRUS (-) DNA CONTAINING FOREIGN DNA

20 For initial production of a recombinant vesiculovirus, the foreign DNA comprising a sequence encoding the desired antigen is inserted into and/or replaces a region of the vesiculovirus (-) DNA nonessential for replication. Many strategies known in the art can be used in the
25 construction of the vesiculovirus (-) DNA containing the foreign DNA. For example, the relevant sequences of the foreign DNA and of the vesiculovirus (-) DNA can, by techniques known in the art, be cleaved at appropriate sites with restriction endonuclease(s), isolated, and ligated in
30 vitro. If cohesive termini are generated by restriction endonuclease digestion, no further modification of DNA before ligation may be needed. If, however, cohesive termini of the DNA are not available for generation by restriction
35 endonuclease digestion, or different sites other than those available are preferred, any of numerous techniques known in the art may be used to accomplish ligation of the heterologous DNA at the desired sites. In a preferred

embodiment, a desired restriction enzyme site is readily introduced into the desired DNA by amplification of the DNA by use of PCR with primers containing the restriction enzyme site. By way of another example, cleavage with a restriction
5 enzyme can be followed by modification to create blunt ends by digesting back or filling in single-stranded DNA termini before ligation. Alternatively, the cleaved ends of the vesiculovirus (-) DNA or foreign DNA can be "chewed back" using a nuclease such as nuclease Bal 31, exonuclease III,
10 lambda exonuclease, mung bean nuclease, or T4 DNA polymerase exonuclease activity, to name but a few, in order to remove portions of the sequence.

To facilitate insertion of the foreign DNA, an oligonucleotide sequence (a linker) which encodes one or more
15 restriction sites can be inserted in a region of the vesiculovirus (-) DNA (see, e.g., the polylinker in pVSVSS1, Fig. 2) by ligation to DNA termini. A linker may also be used to generate suitable restriction sites in the foreign DNA sequence.

20 Additionally, vesiculovirus (-) DNA or foreign DNA sequences can be mutated *in vitro* or *in vivo* in order to form new restriction endonuclease sites or destroy preexisting ones, to facilitate *in vitro* ligation procedures. Any technique for mutagenesis known in the art can be used,
25 including but not limited to, *in vitro* site-directed mutagenesis (Hutchinson et al., 1978, J. Biol. Chem. 253:6551), chemical mutagenesis, etc.

Sequences of the vesiculovirus (-) DNA that have been undesirably modified by such *in vitro* manipulations can
30 be "restored," if desired, by introduction of appropriate sequences at the desired sites.

The particular strategy for inserting the foreign DNA will depend on the specific vesiculovirus (-) DNA site to be replaced or inserted into, as well as the foreign DNA to
35 be inserted.

The sequences encoding the immunogenic peptides or proteins are preferably present in single copies, but can also be present in multiple copies within the virus genome.

Formation of the desired vesiculovirus (-) DNA
5 containing the foreign DNA can be confirmed by standard methods such as DNA sequence analysis, hybridization analysis, and/or restriction mapping, using methods well known in the art.

Foreign DNA encoding a desired antigen can be
10 obtained from any of numerous sources such as cloned DNA, genomic DNA, or cDNA made from RNA of the desired pathogen or tumor, as the case may be, or chemically synthesized DNA, and manipulated by recombinant DNA methodology well known in the art (see Sambrook et al., 1991, Molecular Cloning, A
15 Laboratory Manual, 2d ed., Cold Spring Harbor Laboratory Press, New York). In a preferred embodiment, polymerase chain reaction (PCR) is used to amplify the desired fragment of foreign DNA from among a crude preparation of DNA or a small sample of the DNA, by standard methods. Appropriate
20 primers for use in PCR can be readily deduced based on published sequences.

In order to generate appropriate DNA fragments, the DNA (e.g., from the pathogen or tumor of interest) may be cleaved at specific sites using various restriction enzymes.
25 Alternatively, one may use DNaseI in the presence of manganese, or mung bean nuclease (McCutchan et al., 1984, Science 225:626), to fragment the DNA, or the DNA can be physically sheared, as for example, by sonication. The linear DNA fragments can then be separated according to size
30 by standard techniques, including, but not limited to, agarose and polyacrylamide gel electrophoresis and column chromatography.

PCR amplification of DNA fragments containing the desired epitope(s) is most preferably carried out, in which
35 the PCR primers contain and thus introduce into the amplified DNA a desired restriction enzyme recognition site. Alternatively, any restriction enzyme or combination of

restriction enzymes may be used to generate DNA fragment(s) containing the desired epitope(s), provided the enzymes do not destroy the immunopotency of the encoded product.

Consequently, many restriction enzyme combinations may be used to generate DNA fragments which, when inserted into the vesiculovirus (-) DNA, are capable of producing recombinant vesiculoviruses that direct the production of the peptide containing the epitope(s).

Once the DNA fragments are generated,

10 identification of the specific fragment containing the desired sequence may be accomplished in a number of ways. For example, if a small amount of the desired DNA sequence or a homologous sequence is previously available, it can be used as a labeled probe (e.g., nick translated) to detect the DNA
15 fragment containing the desired sequence, by nucleic acid hybridization. Alternatively, if the sequence of the derived gene or gene fragment is known, isolated fragments or portions thereof can be sequenced by methods known in the art, and identified by a comparison of the derived sequence
20 to that of the known DNA or protein sequence. Alternatively, the desired fragment can be identified by techniques including but not limited to mRNA selection, making cDNA to the identified mRNA, chemically synthesizing the gene sequence (provided the sequence is known), or selection on
25 the basis of expression of the encoded protein (e.g., by antibody binding) after "shotgun cloning" of various DNA fragments into an expression system.

The sequences encoding peptides to be expressed in recombinant vesiculoviruses according to the present
30 invention, whether produced by recombinant DNA methods, chemical synthesis, or purification techniques, include but are not limited to sequences encoding all or part (fragments) of the amino acid sequences of pathogen-specific and tumor-specific antigens, as well as other derivatives and
35 analogs thereof displaying the antigenicity or immunogenicity thereof. Derivatives or analogs of antigens can be tested

for the desired activity by procedures known in the art, including but not limited to standard immunoassays.

In particular, antigen derivatives can be made by altering the encoding antigen nucleotide sequences by
5 substitutions, additions or deletions that do not destroy the antigenicity or immunogenicity of the antigen. For example, due to the degeneracy of nucleotide coding sequences, other DNA sequences which encode substantially the same amino acid sequence as a native antigen gene or portion thereof may be
10 used in the practice of the present invention. Other examples may include but are not limited to nucleotide sequences comprising all or portions of genes or cDNAs which are altered by the substitution of different codons that encode a functionally equivalent amino acid residue within
15 the sequence, thus producing a silent change. For example, one or more amino acid residues within the sequence can be substituted by another amino acid of a similar polarity which acts as a functional equivalent, resulting in a silent alteration. Substitutes for an amino acid within the
20 sequence may be selected from other members of the class to which the amino acid belongs. For example, the nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine. The polar neutral amino acids include glycine,
25 serine, threonine, cysteine, tyrosine, asparagine, and glutamine. The positively charged (basic) amino acids include arginine, lysine, and histidine. The negatively charged (acidic) amino acids include aspartic and glutamic acid.

30 The antigen derivatives and analogs can be produced by various methods known in the art. For example, a cloned gene sequence can be modified by any of numerous strategies known in the art (Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, 2d ed., Cold Spring Harbor Laboratory,
35 Cold Spring Harbor, New York). The sequence can be cleaved at appropriate sites with restriction endonuclease(s), followed by further enzymatic modification if desired,

isolated, and ligated *in vitro*. In the production of the gene encoding a derivative or analog of an antigen, care should be taken to ensure that the modified gene remains within the same translational reading frame as the antigen,
5 uninterrupted by translational stop signals, in the gene region where the desired epitope(s) are encoded.

Additionally, the antigen-encoding nucleic acid sequence can be mutated *in vitro* or *in vivo*, to create and/or destroy translation, initiation, and/or termination
10 sequences, or to create variations in coding regions and/or form new restriction endonuclease sites or destroy preexisting ones, to facilitate further *in vitro* modification. Any technique for mutagenesis known in the art can be used, including but not limited to, *in vitro* site-
15 directed mutagenesis (Hutchinson, C., et al., 1978, J. Biol. Chem 253:6551), use of TAB® linkers (Pharmacia), etc.

In another specific embodiment, the encoded antigen derivative is a chimeric, or fusion, protein comprising a first protein or fragment thereof fused to a second,
20 different amino acid sequence. Such a chimeric protein is encoded by a chimeric nucleic acid in which the two coding sequences are joined inframe. Such a chimeric product can be made by ligating the appropriate nucleic acid sequences encoding the desired amino acid sequences to each other by
25 methods known in the art, in the proper coding frame. In a specific embodiment, a fusion protein is produced in which the first protein sequence contains an epitope of an antigen, and the second protein sequence contains an epitope of a different antigen.

30 Derivatives and fragments of known antigens can be readily tested by standard immunoassay techniques to ascertain if they display the desired immunogenicity or antigenicity, rendering a DNA sequence encoding such a fragment or derivative suitable for insertion into the
35 vesiculovirus (-) DNA.

A DNA sequence encoding an epitope that is a hapten, i.e., a molecule that is antigenic in that it can

react selectively with cognate antibodies, but not immunogenic in that it cannot elicit an immune response when administered without adjuvants or carrier proteins, can also be isolated for use, since it is envisioned that, in particular embodiments, presentation by the vesiculoviruses of the invention can confer immunogenicity to the hapten expressed by the virus.

Once identified and isolated, the foreign DNA containing the sequence(s) of interest is then inserted into the vesiculovirus (-) DNA, for production of a recombinant vesiculovirus.

5.4. PRODUCTION OF RECOMBINANT VESICULOVIRUSES

The recombinant vesiculoviruses of the invention are produced by providing in an appropriate host cell: vesiculovirus (-) DNA, in which regions nonessential for replication have been inserted into or replaced by foreign DNA comprising a sequence encoding an Antigen, and recombinant sources of vesiculovirus N protein, P protein, and L protein. The production is preferably in vitro, in cell culture.

The host cell used for recombinant vesiculovirus production can be any cell in which vesiculoviruses grow, e.g., mammalian cells and some insect (e.g., *Drosophila*) cells. Primary cells, or more preferably, cell lines can be used. A vast number of cell lines commonly known in the art are available for use. By way of example, such cell lines include but are not limited to BHK (baby hamster kidney) cells, CHO (Chinese hamster ovary) cells, HeLA (human) cells, mouse L cells, Vero (monkey) cells, ESK-4, PK-15, EMSK cells, MDCK (Madin-Darby canine kidney) cells, MDBK (Madin-Darby bovine kidney) cells, 293 (human) cells, and Hep-2 cells.

The sources of N, P, and L proteins can be the same or different recombinant nucleic acid(s), encoding and capable of expressing the N, P and L proteins in the host cell in which it is desired to produce recombinant vesiculovirus.

The nucleic acids encoding the N, P and L proteins are obtained by any means available in the art. The N, P and L nucleic acid sequences have been disclosed and can be used. For example, see Genbank accession no. J02428; Rose and Schubert, 1987, in *The Viruses: The Rhabdoviruses*, Plenum Press, NY, pp. 129-166. The sequences encoding the N, P and L genes can also be obtained from plasmid pVSVFL(+), deposited with the ATCC and assigned accession no. 97134, e.g., by PCR amplification of the desired gene (PCR; U.S. Patent Nos. 4,683,202, 4,683,195 and 4,889,818; Gyllenstein et al., 1988, Proc. Natl. Acad. Sci. USA 85:7652-7656; Ochman et al., 1988, Genetics 120:621-623; Loh et al., 1989, Science 243:217-220). If a nucleic acid clone of any of the N, P or L genes is not already available, the clone can be obtained by use of standard recombinant DNA methodology. For example, the DNA may be obtained by standard procedures known in the art by purification of RNA from vesiculoviruses followed by reverse transcription and polymerase chain reaction (Mullis and Faloona, 1987, Methods in Enzymology 155:335-350). Alternatives to isolating an N, P or L gene include, but are not limited to, chemically synthesizing the gene sequence itself. Other methods are possible and within the scope of the invention.

If desired, the identified and isolated gene can then optimally be inserted into an appropriate cloning vector prior to transfer to an expression vector.

Nucleic acids that encode derivatives (including fragments) and analogs of native N, P and L genes, as well as derivatives and analogs of the vesiculovirus (-) DNA can also be used in the present invention, as long as such derivatives and analogs retain function, as exemplified by the ability when used according to the invention to produce a replicable vesiculovirus containing a genomic RNA containing foreign RNA. In particular, derivatives can be made by altering sequences by substitutions, additions, or deletions that provide for functionally active molecules. Furthermore, due to the inherent degeneracy of nucleotide coding sequences,

other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be used in the practice of the methods of the invention. Amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity and/or the amphipathic nature of the residues involved.

The desired N/P/L-encoding nucleic acid is then preferably inserted into an appropriate expression vector, i.e., a vector which contains the necessary elements for the transcription and translation of the inserted protein-coding sequence in the host in which it is desired to produce recombinant vesiculovirus, to create a vector that functions to direct the synthesis of the N/P/L protein that will subsequently assemble with the vesiculovirus genomic RNA containing the foreign sequence (produced in the host cell from antigenomic vesiculovirus (+) RNA produced by transcription of the vesiculovirus (-) DNA). A variety of vector systems may be utilized to express the N, P and L-coding sequences, as well as to transcribe the vesiculovirus (-) DNA containing the foreign DNA, as long as the vector is functional in the host and compatible with any other vector present. Such vectors include but are not limited to bacteriophages, plasmids, or cosmids. In a preferred aspect, a plasmid expression vector is used. The expression elements of vectors vary in their strengths and specificities. Any one of a number of suitable transcription and translation elements may be used, as long as they are functional in the host.

Standard recombinant DNA methods may be used to construct expression vectors containing DNA encoding the N, P, and L proteins, and the vesiculovirus (-) DNA containing the foreign DNA, comprising appropriate transcriptional/translational control signals (see, e.g., Sambrook et al., 1989, *supra*, and methods described hereinabove). (Translational control signals are not needed for transcription of the vesiculovirus (-) DNA, and thus may be omitted from a vector containing the vesiculovirus (-) DNA,

although such signals may be present in the vector and operably linked to other sequences encoding a protein which it is desired to express). Expression may be controlled by any promoter/enhancer element known in the art. Promoters
5 which may be used to control expression can be constitutive or inducible. In a specific embodiment, the promoter is an RNA polymerase promoter.

Transcription termination signals (downstream of the gene), and selectable markers are preferably also
10 included in a plasmid expression vector. In addition to promoter sequences, expression vectors for the N, P, and L proteins preferably contain specific initiation signals for efficient translation of inserted N/P/L sequences, e.g., a ribosome binding site.

15 Specific initiation signals are required for efficient translation of inserted protein coding sequences. These signals include the ATG initiation codon and adjacent sequences. In cases where the entire N, P, or L gene including its own initiation codon and adjacent sequences are
20 inserted into the appropriate vectors, no additional translational control signals may be needed. However, in cases where only a portion of the gene sequence is inserted, exogenous translational control signals, including the ATG initiation codon, must be provided. The initiation codon
25 must furthermore be in phase with the reading frame of the protein coding sequences to ensure translation of the entire insert. These exogenous translational control signals and initiation codons can be of a variety of origins, both natural and synthetic.

30 In a specific embodiment, a recombinant expression vector provided by the invention, encoding an N, P, and/or L protein or functional derivative thereof, comprises the following operatively linked components: a promoter which controls the expression of the N, P, or L protein or
35 functional derivative thereof, a translation initiation signal, a DNA sequence encoding the N, P or L protein or functional derivative thereof, and a transcription

termination signal. In a preferred aspect, the above components are present in 5' to 3' order as listed above.

In another specific embodiment, the gene encoding the N, P, or L protein is inserted downstream of the T7 RNA polymerase promoter from phage T7 gene 10, situated with an A in the -3 position. A T7 RNA polymerase terminator and a replicon are also included in the expression vector. In this embodiment, T7 RNA polymerase is provided to transcribe the N/P/L sequence. The T7 RNA polymerase can be produced from a
10 chromosomally integrated sequence or episomally, and is most preferably provided by intracellular expression from a recombinant vaccinia virus encoding the T7 RNA polymerase (see *infra*). Preferably, the N, P, and L proteins are each encoded by a DNA sequence operably linked to a promoter in an
15 expression plasmid, containing the necessary regulatory signals for transcription and translation of the N, P, and L proteins. Such an expression plasmid preferably includes a promoter, the coding sequence, and a transcription termination/polyadenylation signal, and optionally a
20 selectable marker (e.g., β -galactosidase). The N, P and L proteins can be encoded by the same or different plasmids, or a combination thereof, and preferably are in different plasmids. Less preferably, one or more of the N, P, and L proteins can be expressed intrachromosomally.

25 The cloned sequences comprising the vesiculovirus (-) DNA containing the foreign DNA, and the cloned sequences comprising sequences encoding the N, P, and L proteins can be introduced into the desired host cell by any method known in the art, e.g., transfection, electroporation, infection (when
30 the sequences are contained in, e.g., a viral vector), microinjection, etc.

In a preferred embodiment, DNA comprising vesiculovirus (-) DNA containing foreign DNA encoding an Antigen, operably linked to an RNA polymerase promoter
35 (preferably a bacteriophage RNA polymerase promoter); DNA encoding N, operably linked to the same RNA polymerase promoter; DNA encoding P, operably linked to the same

- polymerase promoter; and DNA encoding L, operably linked to the same polymerase promoter; are all introduced (preferably by transfection) into the same host cell, in which host cell the RNA polymerase has been cytoplasmically provided. The
- 5 RNA polymerase is cytoplasmically provided preferably by expression from a recombinant virus that replicates in the cytoplasm and expresses the RNA polymerase, most preferably a vaccinia virus (see the section hereinbelow), that has been introduced (e.g., by infection) into the same host cell.
- 10 Cytoplasmic provision of RNA polymerase is preferred, since this will result in cytoplasmic transcription and processing, of the VSV (-) DNA comprising the foreign DNA and of the N, P and L proteins, avoiding splicing machinery in the cell nucleus, and thus maximizing proper processing and production
- 15 of N, P and L proteins, and resulting assembly of the recombinant vesiculovirus. For example, vaccinia virus also cytoplasmically provides enzymes for processing (capping and polyadenylation) of mRNA, facilitating proper translation. In a most preferred aspect, T7 RNA polymerase promoters are
- 20 employed, and a cytoplasmic source of T7 RNA polymerase is provided by also introducing into the host cell a recombinant vaccinia virus encoding T7 RNA polymerase into the host cell. Such vaccinia viruses can be obtained by well known methods (see section 5.5, *infra*). In a preferred aspect, a
- 25 recombinant vaccinia virus such as vTF7-3 (Fuerst et al., 1986, Proc. Natl. Acad. Sci. U.S.A. 83:8122-8126) can be used. In a most preferred aspect, the DNA comprising vesiculovirus (-) DNA containing foreign DNA is plasmid pVSVSS1 in which foreign DNA has been inserted into the
- 30 polylinker region.

Alternatively, but less preferably, the RNA polymerase (e.g., T7 RNA polymerase) can be provided by use of a host cell that expresses T7 RNA polymerase from a chromosomally integrated sequence (e.g., originally inserted

35 into the chromosome by homologous recombination), preferably constitutively, or that expresses T7 RNA polymerase episomally, from a plasmid.

In another, less preferred, embodiment, the VSV (-) DNA encoding an Antigen, operably linked to a promoter, can be transfected into a host cell that stably recombinantly expresses the N, P, and L proteins from chromosomally integrated sequences.

The cells are cultured and recombinant vesiculovirus is recovered, by standard methods. For example, and not by limitation, after approximately 24 hours, cells and medium are collected, freeze-thawed, and the lysates clarified to yield virus preparations.

Alternatively, the cells and medium are collected and simply cleared of cells and debris by low-speed centrifugation.

Confirmation that the appropriate foreign sequence is present in the genome of the recombinant vesiculovirus and directs the production of the desired protein(s) in an infected cell, is then preferably carried out. Standard procedures known in the art can be used for this purpose. For example, genomic RNA is obtained from the vesiculovirus by SDS phenol extraction from virus preparations, and can be subjected to reverse transcription (and PCR, if desired), followed by sequencing, Southern hybridization using a probe specific to the foreign DNA, or restriction enzyme mapping, etc. The virus can be used to infect host cells, which can then be assayed for expression of the desired protein by standard immunoassay techniques using an antibody to the protein, or by assays based on functional activity of the protein. Other techniques are known in the art and can be used.

The invention also provides kits for production of recombinant vesiculoviruses. In one embodiment, the kit comprises in one or more (and most preferably, in separate) containers: (a) a first recombinant DNA that can be transcribed in a suitable host cell to produce a vesiculovirus antigenomic (+) RNA in which a portion of the RNA nonessential for replication of the vesiculovirus has been inserted into or replaced by a foreign RNA sequence; (b) a second recombinant DNA comprising a sequence encoding a

vesiculovirus N protein; (c) a third recombinant DNA comprising a sequence encoding a vesiculovirus L protein; and (d) a fourth recombinant DNA comprising a sequence encoding a vesiculovirus P protein. The second, third and fourth
5 recombinant DNAs can be part of the same or different DNA molecules. In a preferred embodiment, the sequences encoding the N, L, and P proteins are each operably linked to a promoter that controls expression of the N, L, and P proteins, respectively, in the suitable host cell. In
10 various embodiments, the kit can contain the various nucleic acids, e.g., plasmid expression vectors, described hereinabove for use in production of recombinant vesiculoviruses.

In another embodiment, a kit of the invention
15 comprises (a) a first recombinant DNA that can be transcribed in a suitable host cell to produce a vesiculovirus antigenomic DNA in which a portion of the RNA nonessential for replication of the vesiculovirus has been inserted into or replaced by a foreign RNA sequence; and (b) a host cell
20 that recombinantly expresses vesiculovirus N, P and L proteins.

In a preferred embodiment, a kit of the invention comprises in separate containers:

(a) a first plasmid comprising the following
25 operatively linked components: (i) a bacteriophage RNA polymerase promoter, (ii) a DNA comprising a sequence capable of being transcribed in a suitable host cell to produce an RNA molecule comprising a vesiculovirus antigenomic RNA in which a portion of the RNA nonessential for replication of
30 the vesiculovirus has been inserted into or replaced by a foreign RNA sequence, and in which the 3' end of the antigenomic RNA is immediately adjacent to a ribozyme sequence that cleaves at the 3' end of the antigenomic RNA, and (iii) a transcriptional termination signal for the
35 bacteriophage RNA polymerase; and

(b) a second plasmid comprising the following operatively linked components: (i) the bacteriophage RNA

polymerase promoter, (ii) a DNA comprising a sequence encoding the vesiculovirus N protein, and (ii) a transcriptional termination signal for the bacteriophage RNA polymerase; and

5 (c) a third plasmid comprising the following operatively linked components: (i) the bacteriophage RNA polymerase promoter, (ii) a DNA comprising a sequence encoding the vesiculovirus P protein, and (ii) a transcriptional termination signal for the bacteriophage RNA
10 polymerase; and

(d) a fourth plasmid comprising the following operatively linked components: (i) the bacteriophage RNA polymerase promoter, (ii) a DNA comprising a sequence encoding the vesiculovirus L protein, and (ii) a
15 transcriptional termination signal for the bacteriophage RNA polymerase.

In another embodiment, a kit of the invention further comprises in a separate container a recombinant vaccinia virus encoding and capable of expressing the
20 bacteriophage RNA polymerase.

In a preferred embodiment, the components in the containers are in purified form.

25 5.4.1. RECOMBINANT VACCINIA VIRUSES
ENCODING AND CAPABLE OF
EXPRESSING FOREIGN RNA POLYMERASES

In a preferred aspect of the invention, transcription of the vesiculovirus (-) DNA containing the foreign DNA encoding an Antigen, and/or transcription of the DNA encoding the N, P, and L proteins in the host cell, is
30 controlled by an RNA polymerase promoter (preferably one in which the RNA polymerase is not endogenous to the host cell), and the RNA polymerase (that initiates transcription from the promoter) is recombinantly provided in the host cell by expression from a recombinant vaccinia virus. DNA sequences
35 encoding RNA polymerases are well known and available in the

art and can be used. For example, phage DNA can be obtained and PCR used to amplify the desired polymerase gene.

Insertion of the desired recombinant DNA sequence encoding and capable of expressing the RNA polymerase into a
5 vaccinia virus for expression by the vaccinia virus is preferably accomplished by first inserting the DNA sequence into a plasmid vector which is capable of subsequent transfer to a vaccinia virus genome by homologous recombination. Thus, in a preferred aspect of the invention for constructing
10 the recombinant vaccinia viruses, the desired DNA sequence encoding the polymerase is inserted, using recombinant DNA methodology (see Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, 2d ed., Cold Spring Harbor Laboratory, Cold Spring Harbor, New York) into an insertion (preferably,
15 plasmid) vector flanked by (preferably) nonessential vaccinia DNA sequences, thus providing for subsequent transfer of its chimeric gene(s) into vaccinia virus by homologous recombination. The sequences are placed in the vector such that they can be expressed under the control of a promoter
20 functional in vaccinia virus.

Expression of foreign DNA in recombinant vaccinia viruses requires the positioning of promoters functional in vaccinia so as to direct the expression of the protein-coding polymerase DNA sequences. Plasmid insertion vectors have
25 been constructed to insert chimeric genes into vaccinia virus for expression therein. Examples of such vectors are described by Mackett (Mackett et al., 1984. J. Virol. 49:857-864). The DNA encoding the polymerase is inserted into a suitable restriction endonuclease cloning site. In addition
30 to plasmid insertion vectors, insertion vectors based on single-stranded M13 bacteriophage DNA (Wilson et al., 1986, Gene 49:207-213) can be used.

The inserted polymerase DNA should preferably not contain introns, and insertion should preferably be so as to
35 place the coding sequences in close proximity to the promoter, with no other start codons in between the initiator ATG and the 5' end of the transcript.

The plasmid insertion vector should contain transcriptional and translational regulatory elements that are active in vaccinia virus. The plasmid should be configured so that the polymerase sequences are under the control of a promoter active in vaccinia virus. Promoters which can be used in the insertion vectors include but are not limited to the vaccinia virus thymidine kinase (TK) promoter, the 7.5K promoter (Cochran et al., 1985, J. Virol. 54:30-37), the 11K promoter (European Patent Publication 0198328), the F promoter (Paoletti et al., 1984, Proc. Natl. Acad. Sci. USA 81:193-197), and various early and late vaccinia promoters (see Moss, 1990, Virology, 2d ed., ch. 74, Fields et al., eds., Raven Press, Ltd., New York, pp. 2079-2111).

In a specific embodiment, the plasmid insertion vector contains (for eventual transfer into vaccinia virus) a T7 RNA polymerase coding sequence under the control of a promoter active in vaccinia virus. In another specific embodiment, a plasmid insertion vector contains a co-expression system consisting of divergently oriented promoters, one directing transcription of the polymerase sequences, the other directing transcription of a reporter gene or selectable marker, to facilitate detection or selection of the eventual recombinant vaccinia virus (see, e.g., Fuerst et al., 1987, Mol. Cell. Biol. 5:1918-1924).

As described supra, the plasmid insertion vector contains at least one set of polymerase coding sequences operatively linked to a promoter, flanked by sequences preferably nonessential for vaccinia viral replication. Such nonessential sequences include but are not limited to the TK gene (Mackett et al., 1984, J. Virol. 49:857-864), the vaccinia HindIII-F DNA fragment (Paoletti et al., 1984, Proc. Natl. Acad. Sci. USA 81:193-197), the vaccinia growth factor gene situated within both terminal repeats (Buller et al., 1988, J. Virol. 62:866-874), the N2 and M1 genes (Tamin et al., 1988, Virology 165:141-150), the M1 subunit of the ribonucleotide reductase gene in the vaccinia HindIII-I DNA

fragment (Child et al., 1990, Virology 174:625-629), the vaccinia hemagglutinin (Shida et al., 1988, J. Virol. 62:4474-4480), vaccinia 14 kD fusion protein gene (Rodriguez et al., 1989, Proc. Natl. Acad. Sci. USA 86:1287-1291), etc. 5 (see also Buller and Palumbo, 1991, Microbiol. Rev. 55(1):80-122). TK sequences are preferred for use; use of such sequences results in the generation of TK⁻ recombinant viruses.

Recombinant vaccinia viruses are preferably 10 produced by transfection of the recombinant insertion vectors containing the polymerase sequences into cells previously infected with vaccinia virus. Alternatively, transfection can take place prior to infection with vaccinia virus. Homologous recombination takes place within the infected 15 cells and results in the insertion of the foreign gene into the viral genome, in the region corresponding to the insertion vector flanking regions. The infected cells can be screened using a variety of procedures such as immunological techniques, DNA plaque hybridization, or genetic selection 20 for recombinant viruses which subsequently can be isolated. These vaccinia recombinants preferably retain their essential functions and infectivity and can be constructed to accommodate up to approximately 35 kilobases of foreign DNA.

Transfections may be performed by procedures known 25 in the art, for example, a calcium chloride-mediated procedure (Mackett et al., 1985, The construction and characterization of vaccinia virus recombinants expressing foreign genes, in *DNA Cloning*, Vol. II, Rickwood and Hames (eds.), IRL Press, Oxford-Washington, D.C.) or a 30 liposome-mediated procedure (Rose et al., 1991, Biotechniques 10:520-525).

Where, as is preferred, flanking TK sequences are used to promote homologous recombination, the resulting recombinant viruses thus have a disrupted TK region, 35 permitting them to grow on a TK⁻ host cell line such as Rat2 (ATCC Accession No. CRL 1764) in the presence of

5-bromo-2'-deoxyuridine (BUDR), under which conditions non-recombinant (TK⁺) viruses will not grow.

In another embodiment, recombinant vaccinia viruses of the invention can be made by *in vitro* cloning, and then
5 packaging with a poxvirus sensitive to a selection condition, rather than by homologous recombination (see International Publication No. WO 94/12617 dated June 9, 1994). For example, the HBV DNA sequences can be inserted into vaccinia genomic DNA using standard recombinant DNA techniques in
10 *vitro*; this recombinant DNA can then be packaged in the presence of a "helper" poxvirus such as a temperature sensitive vaccinia virus mutant or a fowlpox virus which can be selected against under the appropriate conditions.

Various vaccinia virus strains known in the art can
15 be used to generate the recombinant viruses of the invention. A preferred vaccinia virus is the New York City Department of Health Laboratories strain, prepared by Wyeth (available from the American Type Culture Collection (ATCC), Accession No. VR-325). Other vaccinia strains include but are not limited
20 to the Elstree and Moscow strains, the strain of Rivers (CV-1 and CV-2), and the LC16m8 strain of Hashizume.

Selection of the recombinant vaccinia virus can be by any method known in the art, including hybridization techniques (e.g., using polymerase DNA sequences as a
25 hybridization probe), immunological techniques (e.g., assay for binding to antibodies recognizing the encoded polymerase epitope(s)), etc. In a preferred aspect where TK flanking sequences are used in the insertion vector, selection is for TK⁻ recombinants, as described above; screening for the
30 correct recombinant can then be carried out by standard molecular analyses. In many preferred aspects, the method of choice for selection is dictated by the selectable marker in an insertion vector used to generate the recombinant viruses.

The selected recombinant vaccinia virus is then
35 generally plaque-purified, and preferably subjected to standard nucleic acid and protein analyses to verify its

identity and purity, and expression of the inserted polymerase.

5.5. LARGE SCALE GROWTH AND PURIFICATION OF RECOMBINANT REPLICABLE VESICULOVIRUSES

5 The recovered recombinant vesiculovirus, after plaque-purification, can then be grown to large numbers, by way of example, as follows. Virus from a single plaque ($\sim 10^6$ pfu) is recovered and used to infect $\sim 10^7$ cells (e.g., BHK cells), to yield, typically, 10 ml at a titer of 10^9 - 10^{10} pfu/ml for a total of approximately 10^{11} pfu. Infection of $\sim 10^{12}$ cells can then be carried out (with a multiplicity of infection of 0.1), and the cells can be grown in suspension culture, large dishes, or roller bottles by standard methods.

15 It is noted that recombinant vesiculoviruses which no longer express the extracellular region of the vesiculovirus G protein (which determine host range) and which, instead, express an envelope glycoprotein of a different virus will need to be grown in cells which are susceptible to infection by the different virus (and which cells thus express a receptor promoting infection by a virus expressing the envelope glycoprotein of the different virus). Thus, for example, where the recombinant vesiculovirus expresses the HIV envelope glycoprotein, the virus is grown in $CD4^+$ cells (e.g., $CD4^+$ lymphoid cells).

25 Virus for vaccine preparations can then be collected from culture supernatants, and the supernatants clarified to remove cellular debris. If desired, one method of isolating and concentrating the virus that can be employed is by passage of the supernatant through a tangential flow membrane concentration. The harvest can be further reduced in volume by pelleting through a glycerol cushion and by concentration on a sucrose step gradient. An alternate method of concentration is affinity column purification (Daniel et al., 1988, Int. J. Cancer 41:601-608). However, other methods can also be used for purification (see, e.g., Arthur et al., 1986, J. Cell. Biochem. Suppl. 10A:226), and

any possible modifications of the above procedure will be readily recognized by one skilled in the art. Purification should be as gentle as possible, so as to maintain the integrity of the virus particle.

5

5.6. RECOMBINANT REPLICABLE VESICULOVIRUSES FOR USE AS LIVE VACCINES

In one embodiment of the invention, the recombinant replicable vesiculoviruses that express an immunogenic
10 Antigen are used as live vaccines.

The recombinant vesiculoviruses for use as therapeutic or prophylactic live vaccines according to the invention are preferably somewhat attenuated. Most available strains e.g., laboratory strains of VSV, may be sufficiently
15 attenuated for use. Should additional attenuation be desired, e.g., based on pathogenicity testing in animals, attenuation is most preferably achieved simply by laboratory passage of the recombinant vesiculovirus (e.g., in BHK or any other suitable cell line). Generally, attenuated viruses are
20 obtainable by numerous methods known in the art including but not limited to chemical mutagenesis, genetic insertion, deletion (Miller, 1972, Experiments in Molecular Genetics, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY) or recombination using recombinant DNA methodology (Maniatis et
25 al., 1982, Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY), laboratory selection of natural mutants, etc.

In this embodiment of the invention, a vaccine is formulated in which the immunogen is one or several
30 recombinant vesiculovirus(es), in which the foreign RNA in the genome directs the production of an Antigen in a host so as to elicit an immune (humoral and/or cell mediated) response in the host that is prophylactic or therapeutic. In an embodiment wherein the Antigen displays the antigenicity
35 or immunogenicity of an antigen of a pathogen, administration of the vaccine is carried out to prevent or treat an infection by the pathogen and/or the resultant infectious

disorder and/or other undesirable correlates of infection. In an embodiment wherein the Antigen is a tumor antigen, administration of the vaccine is carried out to prevent or treat tumors (particularly, cancer).

- 5 In a preferred specific embodiment, the recombinant vesiculoviruses are administered prophylactically, to prevent/protect against infection and/or infectious diseases or tumor (e.g., cancer) formation.

- In a specific embodiment directed to therapeutics,
10 the recombinant vesiculoviruses of the invention, encoding immunogenic epitope(s), are administered therapeutically, for the treatment of infection or tumor formation. Administration of such viruses, e.g., to neonates and other human subjects, can be used as a method of immunostimulation,
15 to boost the host's immune system, enhancing cell-mediated and/or humoral immunity, and facilitating the clearance of infectious agents or tumors. The viruses of the invention can be administered alone or in combination with other therapies (examples of anti-viral therapies, including but
20 not limited to α -interferon and vidarabine phosphate; examples of tumor therapy including but not limited to radiation and cancer chemotherapy).

5.7. INACTIVATED RECOMBINANT
25 VESICULOVIRUSES FOR VACCINE USE

- In a specific embodiment, the recombinant replicable vesiculoviruses of the invention are inactivated (i.e., killed, rendered nonreplicable) prior to vaccine use, to provide a killed vaccine. Since the vesiculovirus
30 envelope is highly immunogenic, in an embodiment wherein one or more foreign proteins (e.g., an envelope glycoprotein of a virus other than a vesiculovirus) is incorporated into the vesiculovirus envelope, such a virus, even in killed form, can be effective to provide an immune response against said
35 foreign protein(s) in a host to which it is administered. In a specific embodiment, a multiplicity of Antigens, each displaying the immunogenicity or antigenicity of an envelope

glycoprotein of a different virus, are present in the recombinant vesiculovirus particle.

The inactivated recombinant viruses of the invention differ from defective interfering particles in that, prior to inactivation the virus is replicable (i.e., it encodes all the vesiculovirus proteins necessary to enable it to replicate in an infected cell). Thus, since the virus is originally in a replicable state, it can be easily propagated and grown to large amounts prior to inactivation, to provide a large amount of killed virus for use in vaccines, or for purification of the expressed antigen for use in a subunit vaccine (see Section 5.8, *infra*).

Various methods are known in the art and can be used to inactivate the recombinant replicable vesiculoviruses of the invention, for use as killed vaccines. Such methods include but are not limited to inactivation by use of formalin, betapropiolactone, gamma irradiation, and psoralen plus ultraviolet light.

In a specific embodiment, recombinant vesiculovirus can be readily inactivated by resuspension of purified virions in a suitable concentration of formaldehyde. While 0.8 formaldehyde may be sufficient, verification of the optimum concentration of formaldehyde can be readily determined for a particular virus by titration of serial dilutions of formaldehyde with infectious virus to determine the inactivation curve of formalin for that virus. This technique has been described in detail by Salk and Gori, 1960, Ann. N.Y. Acad. Sci. 83:609-637). By extrapolation to zero, the concentration expected to inactivate the last infectious particle can be estimated. By utilizing a substantially higher concentration, e.g., 4-fold greater than the estimated concentration, complete inactivation can be assured.

Although formalin inactivation alone has proven to be effective, it may be desirable, for safety and regulatory purposes, to kill the virus twice or more, using one or more of the numerous other methods currently known for virus

inactivation. Thus, although not essential, it is contemplated that the virus used in the final formulation will be often inactivated by a second agent after treatment with formalin.

5

5.8. USE OF RECOMBINANT REPLICABLE VESICULOVIRUSES IN THE PRODUCTION OF SUBUNIT VACCINES

Since the recombinant vesiculoviruses of the invention can be propagated and grown to large amounts, where
10 the recombinant vesiculoviruses express an Antigen, growth of such vesiculoviruses provides a method for large scale production and ready purification of the expressed Antigen, particularly when the Antigen is incorporated into the envelope of the recombinant vesiculovirus. In a specific
15 embodiment, the Antigen is all or a portion of an envelope glycoprotein of another virus, e.g., HIV gp160, expressed as a nonfusion protein, or expressed as a fusion to the cytoplasmic domain of a vesiculovirus G protein.

The Antigens thus produced and purified have use in
20 subunit vaccines.

The recombinant vesiculoviruses that express an Antigen can also be used to recombinantly produce the Antigen in infected cells *in vitro*, to provide a source of Antigen for use in immunoassays, e.g., to detect or measure in a
25 sample of body fluid from a vaccinated subject the presence of antibodies to the Antigen, and thus to diagnose infection or the presence of a tumor and/or monitor immune response of the subject subsequent to vaccination.

30

5.9. DETERMINATION OF VACCINE EFFICACY

Immunopotency of the one or more Antigen(s) in its live or inactivated vesiculovirus vaccine formulation, or in
is subunit vaccine formulation, can be determined by
monitoring the immune response of test animals following
35 immunization with the recombinant vesiculovirus(es)
expressing the Antigen(s) or with the subunit vaccine

containing the Antigen, by use of any immunoassay known in the art. Generation of a humoral (antibody) response and/or cell-mediated immunity, may be taken as an indication of an immune response. Test animals may include mice, hamsters, dogs, cats, monkeys, rabbits, chimpanzees, etc., and eventually human subjects.

Methods of introduction of the vaccine may include oral, intracerebral, intradermal, intramuscular, intraperitoneal, intravenous, subcutaneous, intranasal or any other standard routes of immunization. The immune response of the test subjects can be analyzed by various approaches such as: the reactivity of the resultant immune serum to the Antigen, as assayed by known techniques, e.g., enzyme linked immunosorbent assay (ELISA), immunoblots, radioimmunoprecipitations, etc.; or, in the case where the Antigen displays the antigenicity or immunogenicity of a pathogen's antigen, by protection of immunized hosts from infection by the pathogen and/or attenuation of symptoms due to infection by the pathogen in immunized hosts; or, in the case where the antigen displays the antigenicity or immunogenicity of a tumor antigen, by prevention of tumor formation or prevention of metastasis, or by regression, or by inhibition of tumor progression, in immunized hosts.

As one example of suitable animal testing of a live vaccine, live vaccines of the invention may be tested in rabbits for the ability to induce an antibody response to the Antigens. Male specific-pathogen-free (SPF) young adult New Zealand White rabbits may be used. The test group of rabbits each receives approximately 5×10^8 pfu (plaque forming units) of the vaccine. A control group of rabbits receives an injection in 1 mM Tris-HCl pH 9.0 of a non-recombinant vesiculovirus or of a recombinant vesiculovirus which does not express the same Antigen.

Blood samples may be drawn from the rabbits every one or two weeks, and serum analyzed for antibodies to the Antigen(s). The presence of antibodies specific for the Antigen(s) may be assayed, e.g., using an ELISA.

Animals may also be used to test vaccine efficacy (e.g., challenge experiments). For example, in a specific embodiment regarding a live vaccine formulation, monkeys each receive intradermally approximately 5×10^8 pfu of recombinant vesiculovirus. A control monkey receives (control) non-recombinant virus intradermally. Blood is drawn weekly for 12 weeks, and serum is analyzed for antibodies to the Antigen(s).

10 5.10. VACCINE FORMULATION AND ADMINISTRATION

The vaccines of the invention may be multivalent or univalent. Multivalent vaccines are made from recombinant viruses that direct the expression of more than one Antigen, from the same or different recombinant viruses.

15 Many methods may be used to introduce the vaccine formulations of the invention; these include but are not limited to oral, intradermal, intramuscular, intraperitoneal, intravenous, subcutaneous, intranasal routes, and via scarification (scratching through the top layers of skin, 20 e.g., using a bifurcated needle).

The patient to which the vaccine is administered is preferably a mammal, most preferably a human, but can also be a non-human animal including but not limited to cows, horses, sheep, pigs, fowl (e.g., chickens), goats, cats, dogs, 25 hamsters, mice and rats. In the use of a live vesiculovirus vaccine, the patient can be any animal in which vesiculovirus replicates (for example, the above-listed animals).

The virus vaccine formulations of the invention comprise an effective immunizing amount of one or more 30 recombinant vesiculoviruses (live or inactivated, as the case may be) and a pharmaceutically acceptable carrier or excipient. Subunit vaccines comprise an effective immunizing amount of one or more Antigens and a pharmaceutically acceptable carrier or excipient. Pharmaceutically acceptable 35 carriers are well known in the art and include but are not limited to saline, buffered saline, dextrose, water, glycerol, sterile isotonic aqueous buffer, and combinations

thereof. One example of such an acceptable carrier is a physiologically balanced culture medium containing one or more stabilizing agents such as stabilized, hydrolyzed proteins, lactose, etc. The carrier is preferably sterile.
5 The formulation should suit the mode of administration.

The composition, if desired, can also contain minor amounts of wetting or emulsifying agents, or pH buffering agents. The composition can be a liquid solution, suspension, emulsion, tablet, pill, capsule, sustained
10 release formulation, or powder. Oral formulation can include standard carriers such as pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharine, cellulose, magnesium carbonate, etc.

Generally, the ingredients are supplied either
15 separately or mixed together in unit dosage form, for example, as a dry lyophilized powder or water free concentrate in a hermetically sealed container such as an ampoule or sachette indicating the quantity of active agent. Where the composition is administered by injection, an
20 ampoule of sterile diluent can be provided so that the ingredients may be mixed prior to administration.

In a specific embodiment, a lyophilized recombinant vesiculovirus of the invention is provided in a first container; a second container comprises diluent consisting of
25 an aqueous solution of 50% glycerin, 0.25% phenol, and an antiseptic (e.g., 0.005% brilliant green).

The precise dose of virus, or subunit vaccine, to be employed in the formulation will also depend on the route of administration, and the nature of the patient, and should
30 be decided according to the judgment of the practitioner and each patient's circumstances according to standard clinical techniques. An effective immunizing amount is that amount sufficient to produce an immune response to the Antigen in the host to which the recombinant vesiculovirus, or subunit
35 vaccine, is administered.

In a specific embodiment, an effective immunizing amount of a live recombinant vesiculovirus of the present

invention is within the range of 10^3 to 10^9 pfu/dose, more preferably 10^6 to 10^9 pfu/dose. Boosting is possible but not preferred. If boosting is desired, one optionally may boost with the Antigen in purified form rather than using a
5 recombinant vesiculovirus of the invention.

For inactivated recombinant vesiculovirus vaccines, the vaccine formulation comprises an effective immunizing amount of the inactivated virus, preferably in combination with an immunostimulant; and a pharmaceutically acceptable
10 carrier. As used in the present context, "immunostimulant" is intended to encompass any compound or composition which has the ability to enhance the activity of the immune system, whether it be a specific potentiating effect in combination with a specific antigen, or simply an independent effect upon
15 the activity of one or more elements of the immune response. Some of the more commonly utilized immunostimulant compounds in vaccine compositions are the adjuvants alum or muramyl dipeptide (MDP) and its analogues. Methods of utilizing these materials are known in the art, and it is well within
20 the ability of the skilled artisan to determine an optimum amount of stimulant for a given virus vaccine. It may also be desired to use more than one immunostimulant in a given formulation.

The exact amount of inactivated virus utilized in a
25 given preparation is not critical, provided that the minimum amount of virus necessary to provoke an immune response is given. A dosage range of as little as about 10 μ g, up to amount a milligram or more, is contemplated. As one example, in a specific embodiment, individual dosages may range from
30 about 50-650 μ g per immunization.

Use of purified Antigens as subunit vaccines can be carried out by standard methods. For example, the purified protein(s) should be adjusted to an appropriate concentration, formulated with any suitable vaccine adjuvant
35 and packaged for use. Suitable adjuvants may include, but are not limited to: mineral gels, e.g., aluminum hydroxide; surface active substances such as lysolecithin, pluronic

polyols; polyanions; peptides; oil emulsions; alum, and MDP. The immunogen may also be incorporated into liposomes, or conjugated to polysaccharides and/or other polymers for use in a vaccine formulation. In instances where the recombinant
5 Antigen is a hapten, i.e., a molecule that is antigenic in that it can react selectively with cognate antibodies, but not immunogenic in that it cannot elicit an immune response, the hapten may be covalently bound to a carrier or immunogenic molecule; for instance, a large protein such as
10 serum albumin will confer immunogenicity to the hapten coupled to it. The hapten-carrier may be formulated for use as a vaccine.

Effective doses (immunizing amounts) of the vaccines of the invention may also be extrapolated from dose-
15 response curves derived from animal model test systems.

The invention also provides a pharmaceutical pack or kit comprising one or more containers comprising one or more of the ingredients of the vaccine formulations of the invention. Associated with such container(s) can be a notice
20 in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration.

The present invention thus provides a method of
25 immunizing an animal, or treating or preventing various diseases or disorders in an animal, comprising administering to the animal an effective immunizing dose of a vaccine of the present invention.

30 5.11. USE OF ANTIBODIES GENERATED
BY THE VACCINES OF THE INVENTION

The antibodies generated against the Antigen by immunization with the recombinant viruses of the present invention also have potential uses in diagnostic
35 immunoassays, passive immunotherapy, and generation of antiidiotypic antibodies.

The generated antibodies may be isolated by standard techniques known in the art (e.g., immunoaffinity chromatography, centrifugation, precipitation, etc.) and used in diagnostic immunoassays. The antibodies may also be used
5 to monitor treatment and/or disease progression. Any immunoassay system known in the art, such as those listed *supra*, may be used for this purpose including but not limited to competitive and noncompetitive assay systems using techniques such as radioimmunoassays, ELISA (enzyme-linked
10 immunosorbent assays), "sandwich" immunoassays, precipitin reactions, gel diffusion precipitin reactions, immunodiffusion assays, agglutination assays, complement-fixation assays, immunoradiometric assays, fluorescent immunoassays, protein A immunoassays and
15 immunoelectrophoresis assays, to name but a few.

The vaccine formulations of the present invention can also be used to produce antibodies for use in passive immunotherapy, in which short-term protection of a host is achieved by the administration of pre-formed antibody
20 directed against a heterologous organism.

The antibodies generated by the vaccine formulations of the present invention can also be used in the production of antiidiotypic antibody. The antiidiotypic antibody can then in turn be used for immunization, in order
25 to produce a subpopulation of antibodies that bind the initial antigen of the pathogenic microorganism (Jerne, 1974, *Ann. Immunol. (Paris)* 125c:373; Jerne, et al., 1982, *EMBO J.* 1:234).

30 6. RECOMBINANT VESICULAR STOMATITIS
 VIRUSES FROM DNA

We assembled a DNA clone containing the 11,161 nucleotide sequence of the prototype rhabdovirus, vesicular stomatitis virus (VSV), such that it could be transcribed by
35 the bacteriophage T7 RNA polymerase to yield a full-length positive strand RNA complementary to the VSV genome. Expression of this RNA in cells also expressing the VSV

nucleocapsid protein and the two VSV polymerase subunits resulted in production of VSV with the growth characteristics of wild-type VSV. Recovery of virus from DNA was verified by: 1) the presence of two genetic tags
5 generating novel restriction sites in DNA derived from the genome; 2) direct sequencing of the genomic RNA of the recovered virus, and 3), production of a VSV recombinant in which the glycoprotein was derived from a second serotype. The ability to generate VSV from DNA opens numerous
10 possibilities for the genetic analysis of VSV replication. In addition, because VSV can be grown to very high titers and in large quantities with relative ease, one can genetically engineer recombinant VSVs displaying novel antigens. Such modified viruses can be used as vaccines conferring
15 protection against other viruses or pathogenic microorganisms, or to produce immunity in general against an encoded foreign antigen.

5.1.4 MATERIALS AND METHODS

20 **Plasmid Construction.** The plasmid pVSVFL(+) expressing the 11,161 nucleotide positive strand (antigenomic) VSV RNA sequence was constructed from four DNA fragments cloned into pBluescript SK⁺ (Stratagene). The starting plasmid for the construction, pVSVFL(-), expressed
25 the complete negative sense VSV genomic RNA (Indiana serotype) from a T7 promoter. This plasmid was generated in a nine step cloning procedure that involved joining the five original cDNA clones of the VSV mRNAs (Gallione et al., 1981, J. Virol. 39:529-535; Rose and Gallione, 1981, J. Virol.
30 39:519-528; Schubert et al., 1985, Proc. Natl. Acad. Sci. USA 82:7984-7988) with gene junction fragments and terminal fragments. These fragments were generated by reverse transcription and polymerase chain reaction (RT-PCR) (Mullis and Faloona, 1987, Methods in Enzymology 155:335-350) from
35 VSV genomic RNA (M.A. Whitt, R. Burdine, E.A. Stillman and J.K. Rose, manuscript in preparation). To facilitate engineering of the VSV genome and to provide genetic tags,

unique Mlu I and Nhe I restriction enzyme sites were introduced by oligonucleotide-directed mutagenesis into the 5' and 3' non-coding regions flanking the VSV glycoprotein gene prior to construction of the full length genome.

- 5 In the initial step of constructing pVSVFL(+) we used the primers
 (5'CCGGCTCGAGTTGTAATACGACTCACTATAGGGACGAAGACAAACAAACCATTATTAT
 C-3') (SEQ ID NO:38) and (5'GAACTCTCCTCTAGATGAGAAC-3') (SEQ
 ID NO:39) to amplify (Mullis and Faloona, 1987, Methods in
 10 Enzymology 155:335-350) a 2,124 nucleotide fragment from
 pVSVFL(-) (# 1, Fig. 4A). This fragment corresponds to the
 3' end of the VSV genome. The first primer introduced an Xho
 I site and a T7 promoter (underlined) immediately preceding
 the sequence complementary to the 3' end of the VSV genome.
 15 The second primer covered a unique Xba I site present in the
 VSV P gene. The PCR product was digested with Xho I and Xba
 I and cloned into pBluescript SK⁺ (Stratagene) that had been
 digested with Xho I and Xba I. The resulting plasmid
 carrying the sequence corresponding to the 3' end of the VSV
 20 genome preceded by a T7 promoter was designated pBSXX. Note
 that an additional T7 promoter is also present upstream of
 the Xho I site in the vector. Next we generated the sequence
 corresponding to the 5' end of the VSV genome and part of the
 hepatitis delta virus (HDV) ribozyme (Pattnaik et al., 1992,
 25 Cell 69:1011-1120; Perrotta and Been, 1991, Nature
 350:434-436). A 147 nucleotide PCR product (#3, Fig. 4A) was
 amplified from pVSVFL(-) with primers
 (5'AGGTCCGACCGCGAGGAGGTGGAGATGCCATGCCGACCCACGAAGACCACAAAACCAG
 -3') (SEQ ID NO:40) and (5'ATGTTGAAGAGTGACCTACACG-3') (SEQ ID
 30 NO:41). The first primer contained 39 nucleotides of the
 sequence encoding the HDV ribozyme (underlined) followed by
 19 nucleotides complementary to the 3' end of the VSV
 antigenomic RNA. The second primer hybridized within the L
 gene (Fig. 4A). The PCR product was digested with Afl II and
 35 Rsr II and the 80 nucleotide Afl II-Rsr II fragment was
 ligated to a 225 nucleotide Rsr II-Sac I fragment (#4, Fig.
 4A) derived from a plasmid designated pBS-GMG (Stillman et

al., manuscript submitted). Fragment 4 contained the T7 terminator sequence and the remainder of the sequence encoding the HDV ribozyme. Ligated products were digested with Afl II and Sac I and the 305 nucleotide Afl II-Sac I product was cloned into the Afl II and Sac I sites of a modified pBSXX vector that contained an Afl II site inserted at the unique Not I site within the polylinker. This plasmid containing the Afl II-Sac I fragment was designated pBXXAS. To complete the construction, a 10,077 nucleotide Bst 1107 I to Afl II fragment (#2, Fig. 4A) containing 90% of the VSV sequences from pVSVFL(-) was inserted into the unique Bst 1107 I and AflII sites of pBXXAS. The final plasmid was designated pVSVFL(+). The sequences in this plasmid generated by PCR (hatched sequences, Fig. 4B) were determined and contained no errors. We also prepared a plasmid in which the sequence of the VSV Indiana serotype G gene (MluI-NheI) was replaced with the G gene from the New Jersey serotype of VSV (Gallione and Rose, 1983, J. Virol. 46:162-169). This plasmid is called pVSVFL(+)_{INJG} and has only a single T7 promoter.

Transfection and recovery of recombinant VSV. Baby hamster kidney cells (BHK-21, ATCC) were maintained in DME (Dulbecco's modified Eagle's medium) supplemented with 5% fetal bovine serum (FBS). Cells on 10 cm dishes (~70% confluent) were infected at a multiplicity of 10 with VTF7-3 (Fuerst et al., 1986, Proc. Natl. Acad. Sci. USA 83:8122-8126). After 30 min, plasmids encoding the VSV antigenomic RNA and the N, P, and L proteins were transfected into the cells using a calcium phosphate transfection kit according to directions supplied (Stratagene). The coding regions for N, P, and L proteins were each expressed in pBluescript SK(+) from the T7 promoter. Plasmid amounts were 10 µg pVSVFL(+), 5 µg pBS-N, 4 µg pBS-P, and 2 µg pBS-L. After 24-48 h incubation at 37°C in 3% CO₂, cells were scraped from the dish and subjected to three rounds of freeze-thawing (-70°C, 37°C) to release cell-associated virus. Debris was pelleted from the cell lysates by

centrifugation at 1,250 x g for 5 min. Five ml of this lysate was added to approximately 10⁶ BHK cells on a 10 cm plate in 10 ml of DME + 5% FBS. After 48 h the medium was clarified by centrifugation at 1,250 x g for 10 min, and
5 passed through a filter to remove the majority of the vaccinia virus (0.2 μ m pore size, Gelman Sciences). One ml was then added directly to BHK cells that had been plated on a coverslip in a 35 mm dish. After four hours, the cells were fixed in 3% paraformaldehyde and stained with monoclonal
10 antibody I1 to the VSV G₁ protein (Lefrancois and Lyles, 1982, Virology 121:168-174) or 9B5 (Bricker et al., 1987, Virology 161:533-540) to the VSV G_N protein followed by goat anti-mouse rhodamine conjugated antibody (Jackson Research). Cells were then examined by indirect immunofluorescence using a Nikon
15 Microphot-FX microscope equipped with a 40x planapochromat objective. When VSV recovery was successful, 100% of the cells showed the typical bright stain for G protein characteristic of a VSV infection.

Preparation and analysis of VSV RNA and protein.

20 Recombinant VSV and wild-type VSV isolated from single plaques (~10⁵ plaque forming units) were used to infect a monolayer of BHK cells (~80% confluent) on a 10 cm dish in 10 ml DME plus 5% FBS. After 24 h, cell debris and nuclei were removed by centrifugation at 1,250 x g for 5 min, and
25 virus was then pelleted from the medium at 35,000 RPM in a Beckman SW41 rotor for one hour. Virus pellets were resuspended in 0.5 ml 10 mM Tris-HCl, pH 7.4 for protein analysis. For RNA isolation, virus was resuspended in 0.2 ml of 0.5% SDS/0.2M sodium acetate, pH 8.0, followed by
30 extraction with phenol/CHCl₃. RNA was precipitated with 95% ethanol and 5 μ g carrier tRNA. RNA was pelleted by centrifugation at 12,000 x g for 15 min and resuspended in water with 1 unit RNasin (Promega). For analysis of RNA by
RT-PCR, primer pairs flanking either the novel Nhe I or Mlu I
35 sites were used. The first strand DNA synthesis reaction was carried out in 50 μ l of PCR buffer (Promega) containing 5 mM MgCl₂, 1 mM dNTPs, 1 unit RNAs in (Promega), 1 unit avian

myeloblastosis virus reverse transcriptase (AMV RT; Promega) 0.75 μ M primer and approximately 0.25 μ g of VSV genomic RNA. Incubation was at 42°C for 15 min followed by 5 min at 99°C and 5 min at 5°C. PCR was carried out by addition of 0.5 U Taq polymerase, adjustment of MgCl₂ concentration to 1.25 mM, and addition of the second primer (0.75 μ M). The reaction was subjected to 20 thermal cycles: 95°C, 1 min; 60°C 1.5 min. The reaction was then incubated at 60°C for 7 min.

Direct sequencing of VSV genomic RNA was performed according to a previously described protocol based on the dideoxy chain termination method (Mierendorf and Pfeffer, 1987, Methods in Enzymology 152:563-566) except that [α -³²P]dATP (Amersham, Inc.) was used. Each reaction included approximately 0.25 μ g of VSV genomic RNA.

15

6.2. RESULTS

To construct a cDNA clone encoding the entire 11,161 VSV genome, individual cDNA clones of the VSV mRNAs were initially joined using small DNA fragments generated by RT-PCR that covered the four gene junctions. Correct genomic terminal sequences were also generated by RT-PCR of the VSV genome, and these were joined to the other DNAs using restriction sites. This initial clone was constructed with a T7 promoter directing synthesis of the full-length negative strand VSV RNA. Despite numerous attempts, we were unable to recover VSV from cells expressing the VSV genomic RNA and the VSV N, P, and L proteins. The VSV constructed was thus redesigned to express the VSV antigenomic DNA. The construction strategy is described in Materials and Methods and in Fig. 4A-B. The entire VSV sequence as well as a T7 promoter, terminator and HDV ribozyme sequence were cloned in pBluescript SK+ between the Xho I and Sac I sites (Fig. 4B; Fig. 1). An additional T7 promoter is also present upstream of the Xho I site in the plasmid. A slightly different cloning strategy was used to generate plasmids lacking the upstream T7 promoter and VSV has also been recovered from these constructs.

Recovery of VSV from DNA. To determine if we could recover VSV from plasmid DNA, we infected cells with vaccinia vTF7-3 (Fuerst et al., 1986, Proc. Natl. Acad. Sci. USA 83:8122-8126) to provide cytoplasmic T7 RNA polymerase.

5 These cells were then transfected with pVSVFL(+), which expresses the antigenomic VSV RNA from a T7 promoter, and three other plasmids which express the VSV N, P, and L proteins. Expression of the N protein was required to assemble nascent VSV antigenomic RNA into nucleocapsids.

10 Once formed, these nucleocapsids should serve as templates for synthesis of minus strand RNA by the L/P polymerase complex. Encapsidated minus strand RNA should then be a template for transcription, initiating the VSV infectious cycle.

15 The initial recovery experiment employed two 10 cm plates of BHK cells ($\sim 5 \times 10^6$ cells each). At 24 hours after the infection with vTF7-3 and transfection with the four plasmids, cells and medium were frozen and thawed to release any cell-associated VSV, and the clarified lysates were added

20 to fresh BHK cells. After 48 hours, both plates showed severe cytopathic effects that could have been due either to vaccinia virus or to recovered VSV. One ml of each supernatant was then added to small dishes of BHK cells on coverslips. After two hours, one of these coverslips showed

25 rounded cells characteristic of a VSV infection, while the other did not. After 4 hours, cells on both coverslips were fixed, stained with appropriate antibodies, and examined by indirect immunofluorescence microscopy to detect the VSV G protein. All cells on the coverslip showing rounded cells

30 revealed intense fluorescence characteristic of G protein expression during VSV infection (data not shown). Subsequent passaging and analysis described below showed that VSV had been recovered from the transfection. The other coverslip showed no G expression, and no VSV could be recovered after

35 passaging.

Based on the frequency with which rabies virus (Schnell et al., 1994, EMBO J. 13:4195-4203) and VSV

minigenomes (Stillman et al., manuscript submitted) were recovered, we anticipated that recovery of complete VSV, if obtainable, would be a rare event. The initial recovery of VSV from only one of two transfections suggested the possibility that the initial titer in the positive lysate was very low. To examine this titer, we infected BHK cells on coverslips with one tenth of the lysate (1 ml) derived from each initial transfection. After eight hours, the cells were examined for expression of G protein by indirect immunofluorescence. A scan of the entire coverslip revealed no VSV infection from the negative lysate, and only five small areas of infection (2-6 cells each) from the lysate that gave rise to VSV G expression on subsequent passaging. The initial titer was therefore very low as we suspected, and likely represented a total of about 50 infectious particles, probably derived from a VSV infection initiated in only one cell out of 2×10^7 transfected. This low rate of recovery of infectious VSV is typical of that observed in several experiments.

Analysis of viral proteins. Subsequent passages and plaque assays of VSV recovered in three independent experiments revealed plaques that were detectable in less than 16 hours and titers up to 2×10^9 pfu/ml characteristic of VSV. For further verification that VSV had been recovered, the proteins in virus pelleted from the medium were examined by SDS polyacrylamide gel electrophoresis (PAGE). Fig. 5 shows the Coomassie stained gel of proteins of VSV recovered from recombinant DNA (rVSV) and wildtype VSV. The mobilities and relative amounts of the five viral proteins were indistinguishable in the wildtype and recombinant virus.

Identification of sequence tags. In pVSVFL(+), the VSV nucleotide sequence was altered by oligonucleotide-directed mutagenesis to generate unique Mlu I and Nhe I restriction enzyme sites in the 5' and 3' non-coding regions of the glycoprotein gene. To verify that these sites were present in recovered virus, we carried out reverse

transcription of genomic RNA purified from wild-type or recombinant virions using primers upstream of each restriction site. The reverse transcription products were then amplified by PCR using an additional primer downstream of each restriction site. The presence of the genetic tag in the recombinant virus was verified by digestion of the PCR products with the appropriate restriction enzymes. Using this method, the presence of both the Mlu I and Nhe I sequences in the recovered virus RNA was verified, and the results for the Nhe I site are shown in Fig. 6. Sequences from wild-type VSV and recombinant VSV were amplified in parallel and a 620 nucleotide fragment was obtained in both cases (lanes 3 and 5). No product was obtained when reverse transcriptase was omitted from the reactions prior to PCR (lanes 1 and 2), indicating that the PCR product was derived from RNA, not from contaminating DNA. After digestion with Nhe I, expected fragments of 273 and 347 base pairs were obtained from recombinant VSV RNA, while the DNA derived from the wildtype RNA remained undigested (lanes 4 and 6).

Direct sequencing of tagged genomic RNA. The presence of new restriction sites in the DNA generated by PCR provided strong evidence that VSV had been recovered from DNA. To ensure that identification of the genetic tags by PCR had not resulted from inadvertent contamination by plasmid DNA, we carried out direct sequence analysis of the genomic RNA using reverse transcriptase and a primer hybridizing upstream of the Nhe I site. The sequence from the autoradiogram shown in Fig. 7 is in exact agreement with the published sequence of the VSV G mRNA (Rose and Gallione, 1981, J. Virol. 39:519-528) except that the four nucleotide changes used to generate the Nhe I site (GCACAA to GCTAGC) are present. These results show unequivocally that the sequence tag is present in the genomic RNA.

Recombinant VSV Indiana virus carrying the glycoprotein of the New Jersey serotype. There are two serotypes of VSV designated Indiana and New Jersey. The glycoproteins of the two serotypes share approximately 50%

sequence identity (Gallione and Rose, 1983, J. Virol. 46:162-169). In earlier studies we found that the glycoprotein of the New Jersey serotype could complement a mutant of the VSV_I serotype that makes a defective glycoprotein (Whitt et al., 1989, J. Virol. 63:3569-3578). It therefore seemed likely that a recombinant VSV in which the Indiana glycoprotein (G_I) gene was replaced by the New Jersey glycoprotein (G_{NJ}) gene would be viable despite the extensive sequence divergence. To generate such a recombinant, the G_{NJ} cDNA was amplified by PCR using primers that introduced Mlu I and Nhe I sites within the 5' and 3' non-coding regions at each end of the gene. The amplified DNA was cloned into pBluescript and the G_{NJ} protein was expressed in BHK cells using the vaccinia-T7 system. The protein expressed was shown to have membrane fusion activity below pH 6.0 indicating that it was functional (data not shown). This G_{NJ} cDNA was then cloned into the unique Mlu I and Nhe I sites of the full-length construct after removal of sequences encoding G_I. Recombinant VSV was recovered essentially as described above except that the initial transfection was allowed to proceed for 48 hours before the freeze-thaw step. After the first passage, expression of the G_{NJ} protein was verified by indirect immunofluorescence using a monoclonal antibody specific to G_{NJ} (Bricker et al., 1987, Virology 161:533-540). The virus was then plaque purified and grown. To examine the proteins present in the recombinant virus, virus recovered from cells infected with VSV_I, VSV_{NJ}, and the recombinant VSV_{I/NJG} was analyzed by SDS-PAGE followed by Coomassie staining. The VSV_I G, N, P, and M proteins each have mobilities distinct from their VSV_{NJ} counterparts (Fig. 8, lanes 1 and 3). The recombinant VSV_{I/NJG} shows the mobility difference in only the G protein as expected (lane 2). The presence of the novel Nhe I and Mlu I sites in the recombinant was also verified (data not shown).

35

6.3. DISCUSSION

The results presented here establish that infectious VSV can be recovered from recombinant DNA. We believe that expressing the positive strand, antigenomic RNA in the presence of the N, P and L proteins was critical to our success because we have not recovered virus starting with an equivalent construct encoding the genomic RNA.

Why is the initial event of generating VSV so rare, apparently occurring in only 1 in 10^7 to 10^8 transfected cells? One possibility is that our clone contains a sequence error that is only corrected by a rare mutational event. We believe this is not the case because the clone was completely sequenced prior to assembly and differences from published sequences were corrected, or the proteins were shown to be functional in complementation assays. Also, the frequency of recovery is actually higher than expected based on our observations with minigenomes encoding one or two VSV proteins (Stillman et al., manuscript submitted). In these cases we found that a transcribing and replicating minigenome (~2kb RNA) was recovered in about 1 in 10^2 transfected cells expressing the RNA with the N, P and L proteins. Addition of a second cistron (0.85 kb additional RNA) encoding the M protein dropped the recovery rate to approximately 1 in 10^3 transfected cells. If there is a ten-fold drop in recovery rate for each additional kilobase of RNA added, one can easily rationalize an even lower frequency of recovery for the 11, 161 kb genome than we observed. Although these minigenomes encode negative sense RNAs, the comparison of the frequency of recovery to that of the full length plus construct is probably valid because expression of the N, P and L mRNAs would not generate mRNAs complementary to the minigenome.

Although the rate limiting step in generation of infectious VSV is not known, it is likely to be at the level of synthesis and encapsidation of the large antigenomic RNA, which must occur prior to replication and transcription. The complete encapsidation with N protein probably has to occur

on the nascent RNA to protect it from degradation, and the cells in which this occurs must also produce appropriate amounts of L and P proteins to initiate replication. Once this has occurred, however, the transcription and translation of the genome should generate additional N, P, and L proteins as well as the G and M proteins required for budding of infectious virus.

The recovery of VSV from DNA opens numerous aspects of the viral life cycle to genetic analysis. The studies of the genetic signals involved in transcription and replication have so far been confined to analysis of defective RNAs that do not encode viral proteins (Pattnaik et al., 1992, Cell 69:1011-1120; Wertz et al., 1994, Proc. Natl. Acad. Sci. USA 91:8587-8591). These and other signals can be now examined in the context of a VSV infection occurring in the absence of a vaccinia virus infection. The system we have described also provides an opportunity to study the roles of individual viral protein domains and modifications in viral assembly and replication. Previously these analyses have been confined to in vitro systems or to analysis employing the complementation of naturally occurring mutants where synthesis of the mutant protein can complicate the analysis.

Perhaps even more exciting is the ability to use VSV as a vector to express other proteins. The experiment in which we recovered VSV Indiana carrying the glycoprotein from the New Jersey serotype (Fig. 8) illustrates that viable recombinants can be made. For reasons that are unclear the titers of recombinant virus were at least ten-fold lower than those obtained with either parent. The lower titer apparently did not result from a defect in viral assembly because the amounts of proteins in wildtype and recombinant virions at the end of the infection were comparable (Fig. 8). Our previous experiments showed that a foreign glycoprotein carrying the appropriate cytoplasmic tail signal could be incorporated into the VSV envelope (Owens and Rose, 1993, J. Virol. 67:360-365). This suggests that one may generate recombinant VSVs carrying novel proteins in their envelopes.

If these were appropriately attenuated, they can be used as vaccines against other viral diseases.

The truncated genomes of defective interfering particles are replicated and packaged very well, thus we suspect that there will be flexibility in the maximum length of the genome that can be packaged as well. Presumably a longer nucleocapsid can be packaged as a longer bullet-shaped particle. Because of the modular nature of the VSV genome, with conserved gene end and start sequences at the gene junctions (Rose and Schubert, 1987, in *The Viruses: The Rhabdoviruses*, Plenum Publishing Corp., NY, pp. 129-166), it should be relatively easy to engineer additional genes into VSV.

15

7. DEPOSIT OF MICROORGANISMS

Plasmid pVSVFL(+) was deposited on May 2, 1995 with the American Type Culture Collection (ATCC), 1201 Parklawn Drive, Rockville, Maryland 20852, under the provisions of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purposes of Patent Procedures, and assigned accession no. 97134.

The present invention is not to be limited in scope by the microorganism deposited or the specific embodiments described herein. Indeed, various modifications of the invention in addition to those described herein will become apparent to those skilled in the art from the foregoing description and accompanying figures. Such modifications are intended to fall within the scope of the appended claims.

Various publications are cited herein, the disclosures of which are incorporated by reference in their entireties.

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Rose, John K.
- (ii) TITLE OF INVENTION: RECOMBINANT VESICULOVIRUSES AND THEIR USES
- (iii) NUMBER OF SEQUENCES: 41
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: PENNIE & EDMONDS
 - (B) STREET: 1155 Avenue of the Americas
 - (C) CITY: New York
 - (D) STATE: New York
 - (E) COUNTRY: USA
 - (F) ZIP: 10036-2711
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: To Be Assigned
 - (B) FILING DATE: On Even Date Herewith
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Misrock, S. Leslie
 - (B) REGISTRATION NUMBER 18,072
 - (C) REFERENCE/DOCKET NUMBER: 6523-009-228
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (212) 790-9090
 - (B) TELEFAX: (212) 869-9741/8864
 - (C) TELEX: 66141 PENNIE

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14311 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 760..2025
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2092..2886
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2946..3632
- (ix) FEATURE:
 - (A) NAME/KEY: CDS

(B) LOCATION: 3774..5306

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 5429..11755

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CACCTAAATT GTAAGCGTTA ATATTTTGTG AAAATTCGCG TTAAATTTTT GTTAAATCAG	60
CTCATTTTTT AACCAATAGG CCGAAATCGG CAAAATCCCT TATAATCAA AAGAATAGAC	120
CGAGATAGGG TTGAGTGTG TTCCAGTTTG GAACAAGAGT CCACTATTAA AGAACGTGGA	180
CTCCAACGTC AAAGGGCGAA AAACCGTCTA TCAGGGCGAT GGCCCACTAC GTGAACCATC	240
ACCCTAATCA AGTTTTTTGG GGTGAGGTG CCGTAAAGCA CTAAATCGGA ACCCTAAAGG	300
GAGCCCCCGA TTTAGAGCTT GACGGGGAAA GCCGGCGAAC GTGGCGAGAA AGGAAGGGAA	360
GAAAGCGAAA GGAGCGGGCG CTAGGGCGCT GGCAAGTGTA GCGGTCACGC TCGCGTAAC	420
CACCACACCC GCCGCGCTTA ATGCGCGCT ACAGGGCGCG TCCCATTCGC CATTGAGGCT	480
GCGCAACTGT TGGGAAGGGC GATCGGTGCG GGCCTCTTCG CTATTACGCC AGCTGGCGAA	540
AGGGGGATGT GCTGCAAGGC GATTAAGTTG GGTAACGCCA GGGTTTTCCC AGTCACGACG	600
TTGTAAAACG ACGGCCAGTG AATTGTAATA CGACTCACTA TAGGGCGAAT TGGGTACCGG	660
GCCCCCCTC GAGTTGTAAT ACGACTCACT ATAGGGACGA AGACAAACAA ACCATTATTA	720
TJATTAAAAG CCTCAGGAGA AACTTTAACA GTAATCAAA ATG TCT GTT ACA GTC	772
Met Ser Val Thr Val	
1 5	
AAG AGA ATC ATT GAC AAC ACA GTC ATA GTT CCA AAA CTT CCT GCA AAT	822
Lys Arg Ile Ile Asp Asn Thr Val Ile Val Pro Lys Leu Pro Ala Asn	
10 15 20	
GAG GAT CCA GTG GAA TAC CCG GCA GAT TAC TTC AGA AAA TCA AAG GAG	870
Glu Asp Pro Val Glu Tyr Pro Ala Asp Tyr Phe Arg Lys Ser Lys Glu	
25 30 35	
ATT CCT CTT TAC ATC AAT ACT ACA AAA AGT TTG TCA GAT CTA AGA GGA	918
Ile Pro Leu Tyr Ile Asn Thr Thr Lys Ser Leu Ser Asp Leu Arg Gly	
40 45 50	
TAT GTC TAC CAA GGC CTC AAA TCC GGA AAT GTA TCA ATC ATA CAT GTC	966
Tyr Val Tyr Gln Gly Leu Lys Ser Gly Asn Val Ser Ile Ile His Val	
55 60 65	
AAC AGC TAC TTG TAT GGA GCA TTA AAG GAC ATC CGG GGT AAG TTG GAT	1014
Asn Ser Tyr Leu Tyr Gly Ala Leu Lys Asp Ile Arg Gly Lys Leu Asp	
70 75 80 85	
AAA GAT TGG TCA AGT TTC GGA ATA AAC ATC GGG AAA GCA GGG GAT ACA	1062
Lys Asp Trp Ser Ser Phe Gly Ile Asn Ile Gly Lys Ala Gly Asp Thr	
90 95 100	
ATC GGA ATA TTT GAC CTT GTA TCC TTG AAA GCC CTG GAC GGC GTA CTT	1110
Ile Gly Ile Phe Asp Leu Val Ser Leu Lys Ala Leu Asp Gly Val Leu	
105 110 115	
CCA GAT GGA GTA TCG GAT GCT TCC AGA ACC AGC GCA GAT GAC AAA TGG	1158
Pro Asp Gly Val Ser Asp Ala Ser Arg Thr Ser Ala Asp Asp Lys Trp	

120	125	130	
TTG CCT TTG TAT CTA CTT GGC TTA TAC AGA GTG GGC AGA ACA CAA ATG Leu Pro Leu Tyr Leu Leu Gly Leu Tyr Arg Val Gly Arg Thr Gln Met 135 140 145			1206
CCT GAA TAC AGA AAA AAG CTC ATG GAT GGG CTG ACA AAT CAA TGC AAA Pro Glu Tyr Arg Lys Lys Leu Met Asp Gly Leu Thr Asn Gln Cys Lys 150 155 160 165			1254
ATG ATC AAT GAA CAG TTT GAA CCT CTT GTG CCA GAA GGT CGT GAC ATT Met Ile Asn Glu Gln Phe Glu Pro Leu Val Pro Glu Gly Arg Asp Ile 170 175 180			1302
TTT GAT GTG TGG GGA AAT GAC AGT AAT TAC ACA AAA ATT GTC GCT GCA Phe Asp Val Trp Gly Asn Asp Ser Asn Tyr Thr Lys Ile Val Ala Ala 185 190 195			1350
GTG GAC ATG TTC TTC CAC ATG TTC AAA AAA CAT GAA TGT GCC TCG TTC Val Asp Met Phe Phe His Met Phe Lys Lys His Glu Cys Ala Ser Phe 200 205 210			1398
AGA TAC GGA ACT ATT GTT TCC AGA TTC AAA GAT TGT GCT GCA TTG GCA Arg Tyr Gly Thr Ile Val Ser Arg Phe Lys Asp Cys Ala Ala Leu Ala 215 220 225			1446
ACA TTT GGA CAC CTC TGC AAA ATA ACC GGA ATG TCT ACA GAA GAT GTA Thr Phe Gly His Leu Cys Lys Ile Thr Gly Met Ser Thr Glu Asp Val 230 235 240 245			1494
ACG ACC TGG ATC TTG AAC CGA GAA GTT GCA GAT GAA ATG GTC CAA ATG Thr Thr Trp Ile Leu Asn Arg Glu Val Ala Asp Glu Met Val Gln Met 250 255 260			1542
ATG CTT CCA GGC CAA GAA ATT GAC AAG GCG GAT TCA TAC AAG CCT TAT Met Leu Pro Gly Gln Glu Ile Asp Lys Ala Asp Ser Tyr Met Pro Tyr 265 270 275			1590
TTG ATC GAC TTT GGA TTG TCT TCT AAG TCT CCA TAT TCT TCC GTC AAA Leu Ile Asp Phe Gly Leu Ser Ser Lys Ser Pro Tyr Ser Ser Val Lys 280 285 290			1638
AAC CCT GCC TTC CAC TTC TGG GGG CAA TTG ACA GCT CTT CTG CTC AGA Asn Pro Ala Phe His Phe Trp Gly Gln Leu Thr Ala Leu Leu Leu Arg 295 300 305			1686
TCC ACC AGA GCA AGG AAT GCC CGA CAG CCT GAT GAC ATT GAG TAT ACA Ser Thr Arg Ala Arg Asn Ala Arg Gln Pro Asp Asp Ile Glu Tyr Thr 310 315 320 325			1734
TCT CTT ACT ACA GCA GGT TTG TTG TAC GCT TAT GCA GTA GGA TCC TCT Ser Leu Thr Thr Ala Gly Leu Leu Tyr Ala Tyr Ala Val Gly Ser Ser 330 335 340			1782
GCC GAC TTG GCA CAA CAG TTT TGT GTT GGA GAT AAC AAA TAC ACT CCA Ala Asp Leu Ala Gln Gln Phe Cys Val Gly Asp Asn Lys Tyr Thr Pro 345 350 355			1830
GAT GAT AGT ACC GGA GGA TTG ACG ACT AAT GCA CCG CCA CAA GGC AGA Asp Asp Ser Thr Gly Gly Leu Thr Thr Asn Ala Pro Pro Gln Gly Arg 360 365 370			1878
GAT GTG GTC GAA TGG CTC GGA TGG TTT GAA GAT CAA AAC AGA AAA CCG Asp Val Val Glu Trp Leu Gly Trp Phe Glu Asp Gln Asn Arg Lys Pro 375 380 385			1926
ACT CCT GAT ATG ATG CAG TAT GCG AAA AGA GCA GTC ATG TCA CTG CAA			1974

Thr Pro Asp Met Met Gln Tyr Ala Lys Arg Ala Val Met Ser Leu Gln
 390 395 400 405
 GGC CTA AGA GAG AAG ACA ATT GGC AAG TAT GCT AAG TCA GAA TTT GAC 2022
 Gly Leu Arg Glu Lys Thr Ile Gly Lys Tyr Ala Lys Ser Glu Phe Asp
 410 415 420
 AAA TGA CCCTATAATT CTCAGATCAC CTATTATATA TTATGCTACA TATGAAAAAA 2078
 Lys
 ACTAACAGAT ATC ATG GAT AAT CTC ACA AAA GTT CGT GAG TAT CTC AAG 2127
 Met Asp Asn Leu Thr Lys Val Arg Glu Tyr Leu Lys
 1 5 10
 TCC TAT TCT CGT CTG GAT CAG GCG GTA GGA GAG ATA GAT GAG ATC GAA 2175
 Ser Tyr Ser Arg Leu Asp Gln Ala Val Gly Glu Ile Asp Glu Ile Glu
 15 20 25
 GCA CAA CGA GCT GAA AAG TCC AAT TAT GAG TTG TTC CAA GAG GAT GGA 2223
 Ala Gln Arg Ala Glu Lys Ser Asn Tyr Glu Leu Phe Gln Glu Asp Gly
 30 35 40
 GTG GAA GAG CAT ACT AAG CCC TCT TAT TTT CAG GCA GCA GAT GAT TCT 2271
 Val Glu Glu His Thr Lys Pro Ser Tyr Phe Gln Ala Ala Asp Asp Ser
 45 50 55 60
 GAC ACA GAA TCT GAA CCA GAA ATT GAA GAC AAT CAA GGT TTG TAT GCA 2319
 Asp Thr Glu Ser Glu Pro Glu Ile Glu Asp Asn Gln Gly Leu Tyr Ala
 65 70 75
 CCA GAT CCA GAA GCT GAG CAA GTT GAA GGC TTT ATA CAG GGG CCT TTA 2367
 Pro Asp Pro Glu Ala Glu Gln Val Glu Gly Phe Ile Gln Gly Pro Leu
 80 85 90
 GAT GAC TAT GCA GAT GAG GAA GTG GAT GTT GTA TTT ACT TCG GAC TGG 2415
 Asp Asp Tyr Ala Asp Glu Glu Val Asp Val Val Phe Thr Ser Asp Trp
 95 100 105
 AAA CAG CCT GAG CTT GAA TCT GAC GAG CAT GGA AAG ACC TTA CGG TTG 2463
 Lys Gln Pro Glu Leu Glu Ser Asp Glu His Gly Lys Thr Leu Arg Leu
 110 115 120
 ACA TCG CCA GAG GGT TTA AGT GGA GAG CAG AAA TCC CAG TGG CTT TCG 2511
 Thr Ser Pro Glu Gly Leu Ser Gly Glu Gln Lys Ser Gln Trp Leu Ser
 125 130 135 140
 ACG ATT AAA GCA GTC GTG CAA AGT GCC AAA TAC TGG AAT CTG GCA GAG 2559
 Thr Ile Lys Ala Val Val Gln Ser Ala Lys Tyr Trp Asn Leu Ala Glu
 145 150 155
 TGC ACA TTT GAA GCA TCG GGA GAA GGG GTC ATT ATG AAG GAG CGC CAG 2607
 Cys Thr Phe Glu Ala Ser Gly Glu Gly Val Ile Met Lys Glu Arg Gln
 160 165 170
 ATA ACT CCG GAT GTA TAT AAG GTC ACT CCA GTG ATG AAC ACA CAT CCG 2655
 Ile Thr Pro Asp Val Tyr Lys Val Thr Pro Val Met Asn Thr His Pro
 175 180 185
 TCC CAA TCA GAA GCA GTA TCA GAT GTT TGG TCT CTC TCA AAG ACA TCC 2703
 Ser Gln Ser Glu Ala Val Ser Asp Val Trp Ser Leu Ser Lys Thr Ser
 190 195 200
 ATG ACT TTC CAA CCC AAG AAA GCA AGT CTT CAG CCT CTC ACC ATA TCC 2751
 Met Thr Phe Gln Pro Lys Lys Ala Ser Leu Gln Pro Leu Thr Ile Ser
 205 210 215 220

TTG GAT GAA TTG TTC TCA TCT AGA GGA GAG TTC ATC TCT GTC GGA GGT Leu Asp Glu Leu Phe Ser Ser Arg Gly Glu Phe Ile Ser Val Gly Gly 225 230 235	2799
GAC GGA CGA ATG TCT CAT AAA GAG GCC ATC CTG CTC GGC CTG AGA TAC Asp Gly Arg Met Ser His Lys Glu Ala Ile Leu Leu Gly Leu Arg Tyr 240 245 250	2847
AAA AAG TTG TAC AAT CAG GCG AGA GTC AAA TAT TCT CTG TAG Lys Lys Leu Tyr Asn Gln Ala Arg Val Lys Tyr Ser Leu 255 260 265	2889
ACTATGAAAA AAAGTAACAG ATATCACGAT CTAAGTGTTA TCCCAATCCA TTCATC	2945
ATG AGT TCC TTA AAG AAG ATT CTC GGT CTG AAG GGG AAA GGT AAG AAA Met Ser Ser Leu Lys Lys Ile Leu Gly Leu Lys Gly Lys Gly Lys Lys 1 5 10 15	2993
TCT AAG AAA TTA GGG ATC GCA CCA CCC CCT TAT GAA GAG GAC ACT AGC Ser Lys Lys Leu Gly Ile Ala Pro Pro Tyr Glu Glu Asp Thr Ser 20 25 30	3041
ATG GAG TAT GCT CCG AGC GCT CCA ATT GAC AAA TCC TAT TTT GGA GTT Met Glu Tyr Ala Pro Ser Ala Pro Ile Asp Lys Ser Tyr Phe Gly Val 35 40 45	3089
GAC GAG ATG GAC ACC TAT GAT CCG AAT CAA TTA AGA TAT GAG AAA TTC Asp Glu Met Asp Thr Tyr Asp Pro Asn Gln Leu Arg Tyr Glu Lys Phe 50 55 60	3137
TTC TTT ACA GTG AAA ATG ACG GTT AGA TCT AAT CGT CCG TTC AGA ACA Phe Phe Thr Val Lys Met Thr Val Arg Ser Asn Arg Pro Phe Arg Thr 65 70 75 80	3185
TAC TCA GAT GTG GCA GCC GCT GTA TCC CAT TGG GAT CAC ATG TAC ATC Tyr Ser Asp Val Ala Ala Val Ser His Trp Asp His Met Tyr Ile 85 90 95	3233
GGA ATG GCA GGG AAA CGT CCC TTC TAC AAA ATC TTG GCT TTT TTG GGT Gly Met Ala Gly Lys Arg Pro Phe Tyr Lys Ile Leu Ala Phe Leu Gly 100 105 110	3281
TCT TCT AAT CTA AAG GCC ACT CCA GCG GTA TTG GCA GAT CAA GGT CAA Ser Ser Asn Leu Lys Ala Thr Pro Ala Val Leu Ala Asp Gln Gly Gln 115 120 125	3329
CCA GAG TAT CAC ACT CAC TGC GAA GGC AGG GCT TAT TTG CCA CAT AGG Pro Glu Tyr His Thr His Cys Glu Gly Arg Ala Tyr Leu Pro His Arg 130 135 140	3377
ATG GGG AAG ACC CCT CCC ATG CTC AAT GTA CCA GAG CAC TTC AGA AGA Met Gly Lys Thr Pro Pro Met Leu Asn Val Pro Glu His Phe Arg Arg 145 150 155 160	3425
CCA TTC AAT ATA GGT CTT TAC AAG GGA ACG ATT GAG CTC ACA ATG ACC Pro Phe Asn Ile Gly Leu Tyr Lys Gly Thr Ile Glu Leu Thr Met Thr 165 170 175	3473
ATC TAC GAT GAT GAG TCA CTG GAA GCA GCT CCT ATG ATC TGG GAT CAT Ile Tyr Asp Asp Glu Ser Leu Glu Ala Ala Pro Met Ile Trp Asp His 180 185 190	3521
TTC AAT TCT TCC AAA TTT TCT GAT TTC AGA GAG AAG GCC TTA ATG TTT Phe Asn Ser Ser Lys Phe Ser Asp Phe Arg Glu Lys Ala Leu Met Phe 195 200 205	3569
GGC CTG ATT GTC GAG AAA AAG GCA TCT GGA GCG TGG GTC CTG GAT TCT	3617

Gly Leu Ile Val Glu Lys Lys Ala Ser Gly Ala Trp Val Leu Asp Ser
 210 215 220

ATC AGC CAC TTC AAA TGA GCTAGTCTAA CTTCTAGCTT CTGAACAATC 3665
 Ile Ser His Phe Lys
 225

CCCGGTTTAC TCAGTCTCTC CTAATTCCAG CCTCTCGAAC AACTAATATC CTGTCTTTTC 3725

TATCCCTATG AAAAAAATA ACAGAGATCG ATCTGTTTAC GCGTCACT ATG AAG TGC 3782
 Met Lys Cys
 1

CTT TTG TAC TTA GCC TTT TTA TTC ATT GGG GTG AAT TGC AAG TTC ACC 3830
 Leu Leu Tyr Leu Ala Phe Leu Phe Ile Gly Val Asn Cys Lys Phe Thr
 5 10 15

ATA GTT TTT CCA CAC AAC CAA AAA GGA AAC TGG AAA AAT GTT CCT TCT 3878
 Ile Val Phe Pro His Asn Gln Lys Gly Asn Trp Lys Asn Val Pro Ser
 20 25 30 35

AAT TAC CAT TAT TGC CCG TCA AGC TCA GAT TTA AAT TGG CAT AAT GAC 3926
 Asn Tyr His Tyr Cys Pro Ser Ser Ser Asp Leu Asn Trp His Asn Asp
 40 45 50

TTA ATA GGC ACA GCC ATA CAA GTC AAA ATG CCC AAG AGT CAC AAG GCT 3974
 Leu Ile Gly Thr Ala Ile Gln Val Lys Met Pro Lys Ser His Lys Ala
 55 60 65

ATT CAA GCA GAC GGT TGG ATG TGT CAT GCT TCC AAA TGG GTC ACT ACT 4022
 Ile Gln Ala Asp Gly Trp Met Cys His Ala Ser Lys Trp Val Thr Thr
 70 75 80

TGT GAT TTC CGC TGG TAT GGA CCG AAG TAT ATA ACA CAG TCC ATC CGA 4070
 Cys Asp Phe Arg Trp Tyr Gly Pro Lys Tyr Ile Thr Gln Ser Ile Arg
 85 90 95

TCC TTC ACT CCA TCT GTA GAA CAA TGC AAG GAA AGC ATT GAA CAA ACG 4118
 Ser Phe Thr Pro Ser Val Glu Gln Cys Lys Glu Ser Ile Glu Gln Thr
 100 105 110 115

AAA CAA GGA ACT TGG CTG AAT CCA GGC TTC CCT CCT CAA AGT TGT GGA 4166
 Lys Gln Gly Thr Trp Leu Asn Pro Gly Phe Pro Pro Gln Ser Cys Gly
 120 125 130

TAT GCA ACT GTG ACG GAT GCC GAA GCA GTG ATT GTC CAG GTG ACT CCT 4214
 Tyr Ala Thr Val Thr Asp Ala Glu Ala Val Ile Val Gln Val Thr Pro
 135 140 145

CAC CAT GTG CTG GTT GAT GAA TAC ACA GGA GAA TGG GTT GAT TCA CAG 4262
 His His Val Leu Val Asp Glu Tyr Thr Gly Glu Trp Val Asp Ser Gln
 150 155 160

TTC ATC AAC GGA AAA TGC AGC AAT TAC ATA TGC CCC ACT GTC CAT AAC 4310
 Phe Ile Asn Gly Lys Cys Ser Asn Tyr Ile Cys Pro Thr Val His Asn
 165 170 175

TCT ACA ACC TGG CAT TCT GAC TAT AAG GTC AAA GGG CTA TGT GAT TCT 4358
 Ser Thr Thr Trp His Ser Asp Tyr Lys Val Lys Gly Leu Cys Asp Ser
 180 185 190 195

AAC CTC ATT TCC ATG GAC ATC ACC TTC TTC TCA GAG GAC GGA GAG CTA 4406
 Asn Leu Ile Ser Met Asp Ile Thr Phe Phe Ser Glu Asp Gly Glu Leu
 200 205 210

TCA TCC CTG GGA AAG GAG GGC ACA GGG TTC AGA AGT AAC TAC TTT GCT 4454
 Ser Ser Leu Gly Lys Glu Gly Thr Gly Phe Arg Ser Asn Tyr Phe Ala

215	220	225	
TAT GAA ACT GGA GGC AAG GCC TGC AAA ATG CAA TAC TGC AAG CAT TGG Tyr Glu Thr Gly Gly Lys Ala Cys Lys Met Gln Tyr Cys Lys His Trp 230 235 240			4502
GGA GTC AGA CTC CCA TCA GGT GTC TGG TTC GAG ATG GCT GAT AAG GAT Gly Val Arg Leu Pro Ser Gly Val Trp Phe Glu Met Ala Asp Lys Asp 245 250 255			4550
CTC TTT GCT GCA GCC AGA TTC CCT GAA TGC CCA GAA GGG TCA AGT ATC Leu Phe Ala Ala Ala Arg Phe Pro Glu Cys Pro Glu Gly Ser Ser Ile 260 265 270 275			4598
TCT GCT CCA TCT CAG ACC TCA GTG GAT GTA AGT CTA ATT CAG GAC GTT Ser Ala Pro Ser Gln Thr Ser Val Asp Val Ser Leu Ile Gln Asp Val 280 285 290			4646
GAG AGG ATC TTG GAT TAT TCC CTC TGC CAA GAA ACC TGG AGC AAA ATC Glu Arg Ile Leu Asp Tyr Ser Leu Cys Gln Glu Thr Trp Ser Lys Ile 295 300 305			4694
AGA GCG GGT CTT CCA ATC TCT CCA GTG GAT CTC AGC TAT CTT GCT CCT Arg Ala Gly Leu Pro Ile Ser Pro Val Asp Leu Ser Tyr Leu Ala Pro 310 315 320			4742
AAA AAC CCA GGA ACC GGT CCT GCT TTC ACC ATA ATC AAT GGT ACC CTA Lys Asn Pro Gly Thr Gly Pro Ala Phe Thr Ile Ile Asn Gly Thr Leu 325 330 335			4790
AAA TAC TTT GAG ACC AGA TAC ATC AGA GTC GAT ATT GCT GCT CCA ATC Lys Tyr Phe Glu Thr Arg Tyr Ile Arg Val Asp Ile Ala Ala Pro Ile 340 345 350 355			4838
CTC TCA AGA ATG GTC GGA ATG ATC AGT GGA ACT ACC ACA GAA AGG GAA Leu Ser Arg Met Val Gly Met Ile Ser Gly Thr Thr Thr Glu Arg Glu 360 365 370			4886
CTG TGG GAT GAC TGG GCA CCA TAT GAA GAC GTG GAA ATT GGA CCC AAT Leu Trp Asp Asp Trp Ala Pro Tyr Glu Asp Val Glu Ile Gly Pro Asn 375 380 385			4934
GGA GTT CTG AGG ACC AGT TCA GGA TAT AAG TTT CCT TTA TAC ATG ATT Gly Val Leu Arg Thr Ser Ser Gly Tyr Lys Phe Pro Leu Tyr Met Ile 390 395 400			4982
GGA CAT GGT ATG TTG GAC TCC GAT CTT CAT CTT AGC TCA AAG GCT CAG Gly His Gly Met Leu Asp Ser Asp Leu His Leu Ser Ser Lys Ala Gln 405 410 415			5030
GTG TTC GAA CAT CCT CAC ATT CAA GAC GCT GCT TCG CAA CTT CCT GAT Val Phe Glu His Pro His Ile Gln Asp Ala Ala Ser Gln Leu Pro Asp 420 425 430 435			5078
GAT GAG AGT TTA TTT TTT GGT GAT ACT GGG CTA TCC AAA AAT CCA ATC Asp Glu Ser Leu Phe Phe Gly Asp Thr Gly Leu Ser Lys Asn Pro Ile 440 445 450			5126
GAG CTT GTA GAA GGT TGG TTC AGT AGT TGG AAA AGC TCT ATT GCC TCT Glu Leu Val Glu Gly Trp Phe Ser Ser Trp Lys Ser Ser Ile Ala Ser 455 460 465			5174
TTT TTC TTT ATC ATA GGG TTA ATC ATT GGA CTA TTC TTG GTT CTC CGA Phe Phe Phe Ile Ile Gly Leu Ile Ile Gly Leu Phe Leu Val Leu Arg 470 475 480			5222
GTT GGT ATC CAT CTT TGC ATT AAA TTA AAG CAC ACC AAG AAA AGA CAG			5270

Val Gly Ile His Leu Cys Ile Lys Leu Lys His Thr Lys Lys Arg Gln
 485 490 495

ATT TAT ACA GAC ATA GAG ATG AAC CGA CTT GGA AAG TAA CTC AAT CCT 5319
 Ile Tyr Thr Asp Ile Glu Met Asn Arg Leu Gly Lys
 500 505 510

GCTAGCCAGA TTCTTCATGT TTGGACCAAA TCAACTTGTG ATACCATGCT CAAAGAGGCC 5379

TCAATTATAT TTGAGTTTTT AATTTTTATG AAAAAAATA ACAGCAATC ATG GAA 5434
 Met Glu
 1

GTC CAC GAT TTT GAG ACC GAC GAG TTC AAT GAT TTC AAT GAA GAT GAC 5482
 Val His Asp Phe Glu Thr Asp Glu Phe Asn Asp Phe Asn Glu Asp Asp
 5 10 15

TAT GCC ACA AGA GAA TTC CTG AAT CCC GAT GAG CGC ATG ACG TAC TTG 5530
 Tyr Ala Thr Arg Glu Phe Leu Asn Pro Asp Glu Arg Met Thr Tyr Leu
 20 25 30

AAT CAT GCT GAT TAC AAT TTG AAT TCT CCT CTA ATT AGT GAT GAT ATT 5578
 Asn His Ala Asp Tyr Asn Leu Asn Ser Pro Leu Ile Ser Asp Asp Ile
 35 40 45 50

GAC AAT TTG ATC AGG AAA TTC AAT TCT CTT CCG ATT CCC TCG ATG TGG 5626
 Asp Asn Leu Ile Arg Lys Phe Asn Ser Leu Pro Ile Pro Ser Met Trp
 55 60 65

GAT AGT AAG AAC TGG GAT GGA GTT CTT GAG ATG TTA ACA TCA TGT CAA 5674
 Asp Ser Lys Asn Trp Asp Gly Val Leu Glu Met Leu Thr Ser Cys Gln
 70 75 80

GCC AAT CCC ATC TCA ACA TCT CAG ATG CAT AAA TGG ATG GGA AGT TGG 5722
 Ala Asn Pro Ile Ser Thr Ser Gln Met His Lys Trp Met Gly Ser Trp
 85 90 95

TTA ATG TCT GAT AAT CAT GAT GCC AGT CAA GGG TAT AGT TTT TTA CAT 5770
 Leu Met Ser Asp Asn His Asp Ala Ser Gln Gly Tyr Ser Phe Leu His
 100 105 110

GAA GTG GAC AAA GAG GCA GAA ATA ACA TTT GAC GTG GTG GAG ACC TTC 5818
 Glu Val Asp Lys Glu Ala Glu Ile Thr Phe Asp Val Val Glu Thr Phe
 115 120 125 130

ATC CGC GGC TGG GGC AAC AAA CCA ATT GAA TAC ATC AAA AAG GAA AGA 5866
 Ile Arg Gly Trp Gly Asn Lys Pro Ile Glu Tyr Ile Lys Lys Glu Arg
 135 140 145

TGG ACT GAC TCA TTC AAA ATT CTC GCT TAT TTG TGT CAA AAG TTT TTG 5914
 Trp Thr Asp Ser Phe Lys Ile Leu Ala Tyr Leu Cys Gln Lys Phe Leu
 150 155 160

GAC TTA CAC AAG TTG ACA TTA ATC TTA AAT GCT GTC TCT GAG GTG GAA 5962
 Asp Leu His Lys Leu Thr Leu Ile Leu Asn Ala Val Ser Glu Val Glu
 165 170 175

TTG CTC AAC TTG GCG AGG ACT TTC AAA GGC AAA GTC AGA AGA AGT TCT 6010
 Leu Leu Asn Leu Ala Arg Thr Phe Lys Gly Lys Val Arg Arg Ser Ser
 180 185 190

CAT GGA ACG AAC ATA TGC AGG ATT AGG GTT CCC AGC TTG GGT CCT ACT 6058
 His Gly Thr Asn Ile Cys Arg Ile Arg Val Pro Ser Leu Gly Pro Thr
 195 200 205 210

TTT ATT TCA GAA GGA TGG GCT TAC TTC AAG AAA CTT GAT ATT CTA ATG 6106
 Phe Ile Ser Glu Gly Trp Ala Tyr Phe Lys Lys Leu Asp Ile Leu Met

PCT/US96/06053

- 80 -

Met	Asn	Pro	Asn	Thr	Pro	Ile	Pro	Ser	Lys	Lys	Val	Leu	Gln	Thr	Met	
		485					490					495				
TTG	GAC	ACA	AAG	GCT	ACC	AAT	TGG	AAA	GAA	TTT	CTT	AAA	GAG	ATT	GAT	6970
Leu	Asp	Thr	Lys	Ala	Thr	Asn	Trp	Lys	Glu	Phe	Leu	Lys	Glu	Ile	Asp	
	500					505					510					
GAG	AAG	GGC	TTA	GAT	GAT	GAT	GAT	CTA	ATT	ATT	GGT	CTT	AAA	GGA	AAG	7018
Glu	Lys	Gly	Leu	Asp	Asp	Asp	Asp	Leu	Ile	Ile	Gly	Leu	Lys	Gly	Lys	
	515				520					525					530	
GAG	AGG	GAA	CTG	AAG	TTG	GCA	GGT	AGA	TTT	TTC	TCC	CTA	ATG	TCT	TGG	7066
Glu	Arg	Glu	Leu	Lys	Leu	Ala	Gly	Arg	Phe	Phe	Ser	Leu	Met	Ser	Trp	
				535					540					545		
AAA	TTG	CGA	GAA	TAC	TTT	GTA	ATT	ACC	GAA	TAT	TTG	ATA	AAG	ACT	CAT	7114
Lys	Leu	Arg	Glu	Tyr	Phe	Val	Ile	Thr	Glu	Tyr	Leu	Ile	Lys	Thr	His	
			550					555					560			
TTC	GTC	CCT	ATG	TTT	AAA	GGC	CTG	ACA	ATG	GCG	GAC	GAT	CTA	ACT	GCA	7162
Phe	Val	Pro	Met	Phe	Lys	Gly	Leu	Thr	Met	Ala	Asp	Asp	Leu	Thr	Ala	
		565					570					575				
GTC	ATT	AAA	AAG	ATG	TTA	GAT	TCC	TCA	TCC	GGC	CAA	GGA	TTG	AAG	TCA	7210
Val	Ile	Lys	Lys	Met	Leu	Asp	Ser	Ser	Ser	Gly	Gln	Gly	Leu	Lys	Ser	
	580					585					590					
TAT	GAG	GCA	ATT	TGC	ATA	GCC	AAT	CAC	ATT	GAT	TAC	GAA	AAA	TGG	AAT	7258
Tyr	Glu	Ala	Ile	Cys	Ile	Ala	Asn	His	Ile	Asp	Tyr	Glu	Lys	Trp	Asn	
	595				600					605					610	
AAC	CAC	CAA	AGG	AAG	TTA	TCA	AAC	GGC	CCA	GTG	TTC	CGA	GTT	ATG	GGC	7306
Asn	His	Gln	Arg	Lys	Leu	Ser	Asn	Gly	Pro	Val	Phe	Arg	Val	Met	Gly	
				615					620					625		
CAG	TTC	TTA	GGT	TAT	CCA	TCC	TTA	ATC	GAG	AGA	ACT	CAT	GAA	TTT	TTT	7354
Gln	Phe	Leu	Gly	Tyr	Pro	Ser	Leu	Ile	Glu	Arg	Thr	His	Glu	Phe	Phe	
			630					635					640			
GAG	AAA	AGT	CTT	ATA	TAC	TAC	AAT	GGA	AGA	CCA	GAC	TTG	ATG	CGT	GTT	7402
Glu	Lys	Ser	Leu	Ile	Tyr	Tyr	Asn	Gly	Arg	Pro	Asp	Leu	Met	Arg	Val	
		645					650					655				
CAC	AAC	AAC	ACA	CTG	ATC	AAT	TCA	ACC	TCC	CAA	CGA	GTT	TGT	TGG	CAA	7450
His	Asn	Asn	Thr	Leu	Ile	Asn	Ser	Thr	Ser	Gln	Arg	Val	Cys	Trp	Gln	
		660				665					670					
GGA	CAA	GAG	GGT	GGA	CTG	GAA	GGT	CTA	CGG	CAA	AAA	GGA	TGG	ACT	ATC	7498
Gly	Gln	Glu	Gly	Gly	Leu	Glu	Gly	Leu	Arg	Gln	Lys	Gly	Trp	Thr	Ile	
	675				680					685					690	
CTC	AAT	CTA	CTG	GTT	ATT	CAA	AGA	GAG	GCT	AAA	ATC	AGA	AAC	ACT	GCT	7546
Leu	Asn	Leu	Leu	Val	Ile	Gln	Arg	Glu	Ala	Lys	Ile	Arg	Asn	Thr	Ala	
				695				700						705		
GTC	AAA	GTC	TTG	GCA	CAA	GGT	GAT	AAT	CAA	GTT	ATT	TGC	ACA	CAG	TAT	7594
Val	Lys	Val	Leu	Ala	Gln	Gly	Asp	Asn	Gln	Val	Ile	Cys	Thr	Gln	Tyr	
			710					715					720			
AAA	ACG	AAG	AAA	TCG	AGA	AAC	GTT	GTA	GAA	TTA	CAG	GGT	GCT	CTC	AAT	7642
Lys	Thr	Lys	Lys	Ser	Arg	Asn	Val	Val	Glu	Leu	Gln	Gly	Ala	Leu	Asn	
		725					730					735				
CAA	ATG	GTT	TCT	AAT	AAT	GAG	AAA	ATT	ATG	ACT	GCA	ATC	AAA	ATA	GGG	7690
Gln	Met	Val	Ser	Asn	Asn	Glu	Lys	Ile	Met	Thr	Ala	Ile	Lys	Ile	Gly	
		740				745						750				

ACA GGG AAG TTA GGA CTT TTG ATA AAT GAC GAT GAG ACT ATG CAA TCT Thr Gly Lys Leu Gly Leu Leu Ile Asn Asp Asp Glu Thr Met Gln Ser 755 760 765 770	7738
GCA GAT TAC TTG AAT TAT GGA AAA ATA CCG ATT TTC CGT GGA GTG ATT Ala Asp Tyr Leu Asn Tyr Gly Lys Ile Pro Ile Phe Arg Gly Val Ile 775 780 785	7786
AGA GGG TTA GAG ACC AAG AGA TGG TCA CGA GTG ACT TGT GTC ACC AAT Arg Gly Leu Glu Thr Lys Arg Trp Ser Arg Val Thr Cys Val Thr Asn 790 795 800	7834
GAC CAA ATA CCC ACT TGT GCT AAT ATA ATG AGC TCA GTT TCC ACA AAT Asp Gln Ile Pro Thr Cys Ala Asn Ile Met Ser Ser Val Ser Thr Asn 805 810 815	7882
GCT CTC ACC GTA GCT CAT TTT GCT GAG AAC CCA ATC AAT GCC ATG ATA Ala Leu Thr Val Ala His Phe Ala Glu Asn Pro Ile Asn Ala Met Ile 820 825 830	7930
CAG TAC AAT TAT TTT GGG ACA TTT GCT AGA CTC TTG TTG ATG ATG CAT Gln Tyr Asn Tyr Phe Gly Thr Phe Ala Arg Leu Leu Met Met His 835 840 845 850	7978
GAT CCT GCT CTT CGT CAA TCA TTG TAT GAA GTT CAA GAT AAG ATA CCG Asp Pro Ala Leu Arg Gln Ser Leu Tyr Glu Val Gln Asp Lys Ile Pro 855 860 865	8026
GGC TTG CAC AGT TCT ACT TTC AAA TAC GCC ATG TTG TAT TTG GAC CCT Gly Leu His Ser Ser Thr Phe Lys Tyr Ala Met Leu Tyr Leu Asp Pro 870 875 880	8074
TCC ATT GGA GGA GTG TCG GGC ATG TCT TTG TCC AGG TTT TTG ATT AGA Ser Ile Gly Gly Val Ser Gly Met Ser Leu Ser Arg Phe Leu Ile Ala 885 890 895	8122
GCC TTC CCA GAT CCC GTA ACA GAA AGT CTC TCA TTC TGG AGA TTC ATC Ala Phe Pro Asp Pro Val Thr Glu Ser Leu Ser Phe Trp Arg Phe Ile 900 905 910	8170
CAT GTA CAT GCT CGA AGT GAG CAT CTG AAG GAG ATG AGT GCA GTA TTT His Val His Ala Arg Ser Glu His Leu Lys Glu Met Ser Ala Val Phe 915 920 925 930	8218
GGA AAC CCC GAG ATA GCC AAG TTT CGA ATA ACT CAC ATA GAC AAG CTA Gly Asn Pro Glu Ile Ala Lys Phe Arg Ile Thr His Ile Asp Lys Leu 935 940 945	8266
GTA GAA GAT CCA ACC TCT CTG AAC ATC GCT ATG GGA ATG AGT CCA GCG Val Glu Asp Pro Thr Ser Leu Asn Ile Ala Met Gly Met Ser Pro Ala 950 955 960	8314
AAC TTG TTA AAG ACT GAG GTT AAA AAA TGC TTA ATC GAA TCA AGA CAA Asn Leu Leu Lys Thr Glu Val Lys Lys Cys Leu Ile Glu Ser Arg Gln 965 970 975	8362
ACC ATC AGG AAC CAG GTG ATT AAG GAT GCA ACC ATA TAT TTG TAT CAT Thr Ile Arg Asn Gln Val Ile Lys Asp Ala Thr Ile Tyr Leu Tyr His 980 985 990	8410
GAA GAG GAT CGG CTC AGA AGT TTC TTA TGG TCA ATA AAT CCT CTG TTC Glu Glu Asp Arg Leu Arg Ser Phe Leu Trp Ser Ile Asn Pro Leu Phe 995 1000 1005 1010	8458
CCT AGA TTT TTA AGT GAA TTC AAA TCA GGC ACT TTT TTG GGA GTC GCA Pro Arg Phe Leu Ser Glu Phe Lys Ser Gly Thr Phe Leu Gly Val Ala 1015 1020 1025	8506

GAC GGG CTC ATC AGT CTA TTT CAA AAT TCT CGT ACT ATT CGG AAC TCC Asp Gly Leu Ile Ser Leu Phe Gln Asn Ser Arg Thr Ile Arg Asn Ser 1030 1035 1040	8554
TTT AAG AAA AAG TAT CAT AGG GAA TTG GAT GAT TTG ATT GTG AGG AGT Phe Lys Lys Lys Tyr His Arg Glu Leu Asp Asp Leu Ile Val Arg Ser 1045 1050 1055	8602
GAG GTA TCC TCT TTG ACA CAT TTA GGG AAA CTT CAT TTG AGA AGG GGA Glu Val Ser Ser Leu Thr His Leu Gly Lys Leu His Leu Arg Arg Gly 1060 1065 1070	8650
TCA TGT AAA ATG TGG ACA TGT TCA GCT ACT CAT GCT GAC ACA TTA AGA Ser Cys Lys Met Trp Thr Cys Ser Ala Thr His Ala Asp Thr Leu Arg 1075 1080 1085 1090	8698
TAC AAA TCC TGG GGC CGT ACA GTT ATT GGG ACA ACT GTA CCC CAT CCA Tyr Lys Ser Trp Gly Arg Thr Val Ile Gly Thr Thr Val Pro His Pro 1095 1100 1105	8746
TTA GAA ATG TTG GGT CCA CAA CAT CGA AAA GAG ACT CCT TGT GCA CCA Leu Glu Met Leu Gly Pro Gln His Arg Lys Glu Thr Pro Cys Ala Pro 1110 1115 1120	8794
TGT AAC ACA TCA GGG TTC AAT TAT GTT TCT GTG CAT TGT CCA GAC GGG Cys Asn Thr Ser Gly Phe Asn Tyr Val Ser Val His Cys Pro Asp Gly 1125 1130 1135	8842
ATC CAT GAC GTC TTT AGT TCA CGG GGA CCA TTG CCT GCT TAT CTA GGG Ile His Asp Val Phe Ser Ser Arg Gly Pro Leu Pro Ala Tyr Leu Gly 1140 1145 1150	8890
TCT AAA ACA TCT GAA TCT ACA TCT ATT TTG CAG CCT TGG GAA AGG GAA Ser Lys Thr Ser Glu Ser Thr Ser Ile Leu Gln Pro Trp Glu Arg Glu 1155 1160 1165 1170	8938
AGC AAA GTC CCA CTG ATT AAA AGA GCT ACA CGT CTT AGA GAT GCT ATC Ser Lys Val Pro Leu Ile Lys Arg Ala Thr Arg Leu Arg Asp Ala Ile 1175 1180 1185	8986
TCT TGG TTT GTT GAA CCC GAC TCT AAA CTA GCA ATG ACT ATA CTT TCT Ser Trp Phe Val Glu Pro Asp Ser Lys Leu Ala Met Thr Ile Leu Ser 1190 1195 1200	9034
AAC ATC CAC TCT TTA ACA GGC GAA GAA TGG ACC AAA AGG CAG CAT GGG Asn Ile His Ser Leu Thr Gly Glu Glu Trp Thr Lys Arg Gln His Gly 1205 1210 1215	9082
TTC AAA AGA ACA GGG TCT GCC CTT CAT AGG TTT TCG ACA TCT CGG ATG Phe Lys Arg Thr Gly Ser Ala Leu His Arg Phe Ser Thr Ser Arg Met 1220 1225 1230	9130
AGC CAT GGT GGG TTC GCA TCT CAG AGC ACT GCA GCA TTG ACC AGG TTG Ser His Gly Gly Phe Ala Ser Gln Ser Thr Ala Ala Leu Thr Arg Leu 1235 1240 1245 1250	9178
ATG GCA ACT ACA GAC ACC ATG AGG GAT CTG GGA GAT CAG AAT TTC GAC Met Ala Thr Thr Asp Thr Met Arg Asp Leu Gly Asp Gln Asn Phe Asp 1255 1260 1265	9226
TTT TTA TTC CAA GCA ACG TTG CTC TAT GCT CAA ATT ACC ACC ACT GTT Phe Leu Phe Gln Ala Thr Leu Leu Tyr Ala Gln Ile Thr Thr Thr Val 1270 1275 1280	9274
GCA AGA GAC GGA TGG ATC ACC AGT TGT ACA GAT CAT TAT CAT ATT GCC Ala Arg Asp Gly Trp Ile Thr Ser Cys Thr Asp His Tyr His Ile Ala 1285 1290 1295	9322

TGT AAG TCC TGT TTG AGA CCC ATA GAA GAG ATC ACC CTG GAC TCA AGT Cys Lys Ser Cys Leu Arg Pro Ile Glu Glu Ile Thr Leu Asp Ser Ser 1300 1305 1310	9370
ATG GAC TAC ACG CCC CCA GAT GTA TCC CAT GTG CTG AAG ACA TGG AGG Met Asp Tyr Thr Pro Pro Asp Val Ser His Val Leu Lys Thr Trp Arg 1315 1320 1325 1330	9418
AAT GGG GAA GGT TCG TGG GGA CAA GAG ATA AAA CAG ATC TAT CCT TTA Asn Gly Glu Gly Ser Trp Gly Gln Glu Ile Lys Gln Ile Tyr Pro Leu 1335 1340 1345	9466
GAA GGG AAT TGG AAG AAT TTA GCA CCT GCT GAG CAA TCC TAT CAA GTC Glu Gly Asn Trp Lys Asn Leu Ala Pro Ala Glu Gln Ser Tyr Gln Val 1350 1355 1360	9514
GGC AGA TGT ATA GGT TTT CTA TAT GGA GAC TTG GCG TAT AGA AAA TCT Gly Arg Cys Ile Gly Phe Leu Tyr Gly Asp Leu Ala Tyr Arg Lys Ser 1365 1370 1375	9562
ACT CAT GCC GAG GAC AGT TCT CTA TTT CCT CTA TCT ATA CAA GGT CGT Thr His Ala Glu Asp Ser Ser Leu Phe Pro Leu Ser Ile Gln Gly Arg 1380 1385 1390	9610
ATT AGA GGT CGA GGT TTC TTA AAA GGG TTG CTA GAC GGA TTA ATG AGA Ile Arg Gly Arg Gly Phe Leu Lys Gly Leu Leu Asp Gly Leu Met Arg 1395 1400 1405 1410	9658
GCA AGT TGC TGC CAA GTA ATA CAC CGG AGA AGT CTG GCT CAT TTG AAG Ala Ser Cys Cys Gln Val Ile His Arg Arg Ser Leu Ala His Leu Lys 1415 1420 1425	9706
AGG CCG GCC AAC GCA GTG TAC GGA GGT TTG ATT TAC TTG ATT GAT AAA Arg Pro Ala Asn Ala Val Tyr Gly Gly Leu Ile Tyr Leu Ile Asp Lys 1430 1435 1440	9754
TTG AGT GTA TCA CCT CCA TTC CTT TCT CTT ACT AGA TCA GGA CCT ATT Leu Ser Val Ser Pro Pro Phe Leu Ser Leu Thr Arg Ser Gly Pro Ile 1445 1450 1455	9802
AGA GAC GAA TTA GAA ACG ATT CCC CAC AAG ATC CCA ACC TCC TAT CCG Arg Asp Glu Leu Glu Thr Ile Pro His Lys Ile Pro Thr Ser Tyr Pro 1460 1465 1470	9850
ACA AGC AAC CGT GAT ATG GGG GTG ATT GTC AGA AAT TAC TTC AAA TAC Thr Ser Asn Arg Asp Met Gly Val Ile Val Arg Asn Tyr Phe Lys Tyr 1475 1480 1485 1490	9898
CAA TGC CGT CTA ATT GAA AAG GGA AAA TAC AGA TCA CAT TAT TCA CAA Gln Cys Arg Leu Ile Glu Lys Gly Lys Tyr Arg Ser His Tyr Ser Gln 1495 1500 1505	9946
TTA TGG TTA TTC TCA GAT GTC TTA TCC ATA GAC TTC ATT GGA CCA TTC Leu Trp Leu Phe Ser Asp Val Leu Ser Ile Asp Phe Ile Gly Pro Phe 1510 1515 1520	9994
TCT ATT TCC ACC ACC CTC TTG CAA ATC CTA TAC AAG CCA TTT TTA TCT Ser Ile Ser Thr Thr Leu Leu Gln Ile Leu Tyr Lys Pro Phe Leu Ser 1525 1530 1535	10042
GGG AAA GAT AAG AAT GAG TTG AGA GAG CTG GCA AAT CTT TCT TCA TTG Gly Lys Asp Lys Asn Glu Leu Arg Glu Leu Ala Asn Leu Ser Ser Leu 1540 1545 1550	10090
CTA AGA TCA GGA GAG GGG TGG GAA GAC ATA CAT GTG AAA TTC TTC ACC Leu Arg Ser Gly Glu Gly Trp Glu Asp Ile His Val Lys Phe Phe Thr 1555 1560 1565 1570	10138

AAG GAC ATA TTA TTG TGT CCA GAG GAA ATC AGA CAT GCT TGC AAG TTC	10186
Lys Asp Ile Leu Leu Cys Pro Glu Glu Ile Arg His Ala Cys Lys Phe	
1575 1580 1585	
GGG ATT GCT AAG GAT AAT AAT AAA GAC ATG AGC TAT CCC CCT TGG GGA	10234
Gly Ile Ala Lys Asp Asn Asn Lys Asp Met Ser Tyr Pro Pro Trp Gly	
1590 1595 1600	
AGG GAA TCC AGA GGG ACA ATT ACA ACA ATC CCT GTT TAT TAT ACG ACC	10282
Arg Glu Ser Arg Gly Thr Ile Thr Thr Ile Pro Val Tyr Tyr Thr Thr	
1605 1610 1615	
ACC CCT TAC CCA AAG ATG CTA GAG ATG CCT CCA AGA ATC CAA AAT CCC	10330
Thr Pro Tyr Pro Lys Met Leu Glu Met Pro Pro Arg Ile Gln Asn Pro	
1620 1625 1630	
CTG CTG TCC GGA ATC AGG TTG GGC CAA TTA CCA ACT GGC GCT CAT TAT	10378
Leu Leu Ser Gly Ile Arg Leu Gly Gln Leu Pro Thr Gly Ala His Tyr	
1635 1640 1645 1650	
AAA ATT CGG AGT ATA TTA CAT GGA ATG GGA ATC CAT TAC AGG GAC TTC	10426
Lys Ile Arg Ser Ile Leu His Gly Met Gly Ile His Tyr Arg Asp Phe	
1655 1660 1665	
TTG AGT TGT GGA GAC GGC TCC GGA GGG ATG ACT GCT GCA TTA CTA CGA	10474
Leu Ser Cys Gly Asp Gly Ser Gly Gly Met Thr Ala Ala Leu Leu Arg	
1670 1675 1680	
GAA AAT GTG CAT AGC AGA GGA ATA TTC AAT AGT CTG TTA GAA TTA TCA	10522
Glu Asn Val His Ser Arg Gly Ile Phe Asn Ser Leu Leu Glu Leu Ser	
1685 1690 1695	
GGG TCA GTC ATG CGA GGC GCC TCT CCT GAG CCC CCC AGT GCC CTA GAA	10570
Gly Ser Val Met Arg Gly Ala Ser Pro Glu Pro Pro Ser Ala Leu Glu	
1700 1705 1710	
ACT TTA GGA GGA GAT AAA TCG AGA TGT GTA AAT GGT GAA ACA TGT TGG	10618
Thr Leu Gly Gly Asp Lys Ser Arg Cys Val Asn Gly Glu Thr Cys Trp	
1715 1720 1725 1730	
GAA TAT CCA TCT GAC TTA TGT GAC CCA AGG ACT TGG GAC TAT TTC CTC	10666
Glu Tyr Pro Ser Asp Leu Cys Asp Pro Arg Thr Trp Asp Tyr Phe Leu	
1735 1740 1745	
CGA CTC AAA GCA GGC TTG GGG CTT CAA ATT GAT TTA ATT GTA ATG GAT	10714
Arg Leu Lys Ala Gly Leu Gly Leu Gln Ile Asp Leu Ile Val Met Asp	
1750 1755 1760	
ATG GAA GTT CGG GAT TCT TCT ACT AGC CTG AAA ATT GAG ACG AAT GTT	10762
Met Glu Val Arg Asp Ser Ser Thr Ser Leu Lys Ile Glu Thr Asn Val	
1765 1770 1775	
AGA AAT TAT GTG CAC CGG ATT TTG GAT GAG CAA GGA GTT TTA ATC TAC	10810
Arg Asn Tyr Val His Arg Ile Leu Asp Glu Gln Gly Val Leu Ile Tyr	
1780 1785 1790	
AAG ACT TAT GGA ACA TAT ATT TGT GAG AGC GAA AAG AAT GCA GTA ACA	10858
Lys Thr Tyr Gly Thr Tyr Ile Cys Glu Ser Glu Lys Asn Ala Val Thr	
1795 1800 1805 1810	
ATC CTT GGT CCC ATG TTC AAG ACG GTC GAC TTA GTT CAA ACA GAA TTT	10906
Ile Leu Gly Pro Met Phe Lys Thr Val Asp Leu Val Gln Thr Glu Phe	
1815 1820 1825	
AGT AGT TCT CAA ACG TCT GAA GTA TAT ATG GTA TGT AAA GGT TTG AAG	10954
Ser Ser Ser Gln Thr Ser Glu Val Tyr Met Val Cys Lys Gly Leu Lys	
1830 1835 1840	

AAA TTA ATC GAT GAA CCC AAT CCC GAT TGG TCT TCC ATC AAT GAA TCC Lys Leu Ile Asp Glu Pro Asn Pro Asp Trp Ser Ser Ile Asn Glu Ser 1845 1850 1855	11002
TGG AAA AAC CTG TAC GCA TTC CAG TCA TCA GAA CAG GAA TTT GCC AGA Trp Lys Asn Leu Tyr Ala Phe Gln Ser Ser Glu Gln Glu Phe Ala Arg 1860 1865 1870	11050
GCA AAG AAG GTT AGT ACA TAC TTT ACC TTG ACA GGT ATT CCC TCC CAA Ala Lys Lys Val Ser Thr Tyr Phe Thr Leu Thr Gly Ile Pro Ser Gln 1875 1880 1885 1890	11098
TTC ATT CCT GAT CCT TTT GTA AAC ATT GAG ACT ATG CTA CAA ATA TTC Phe Ile Pro Asp Pro Phe Val Asn Ile Glu Thr Met Leu Gln Ile Phe 1895 1900 1905	11146
GGA GTA CCC ACG GGT GTG TCT CAT GCG GCT GCC TTA AAA TCA TCT GAT Gly Val Pro Thr Gly Val Ser His Ala Ala Ala Leu Lys Ser Ser Asp 1910 1915 1920	11194
AGA CCT GCA GAT TTA TTG ACC ATT AGC CTT TTT TAT ATG GCG ATT ATA Arg Pro Ala Asp Leu Leu Thr Ile Ser Leu Phe Tyr Met Ala Ile Ile 1925 1930 1935	11242
TCG TAT TAT AAC ATC AAT CAT ATC AGA GTA GGA CCG ATA CCT CCG AAC Ser Tyr Tyr Asn Ile Asn His Ile Arg Val Gly Pro Ile Pro Pro Asn 1940 1945 1950	11290
CCC CCA TCA GAT GGA ATT GCA CAA AAT GTG GGG ATC GCT ATA ACT GGT Pro Pro Ser Asp Gly Ile Ala Gln Asn Val Gly Ile Ala Ile Thr Gly 1955 1960 1965 1970	11338
ATA AGC TTT TGG CTG AGT TTG ATG GAG AAA GAC ATT CCA CTA TAT CAA Ile Ser Phe Trp Leu Ser Leu Met Glu Lys Asp Ile Pro Leu Tyr Gln 1975 1980 1985	11386
CAG TGT TTA GCA GTT ATC CAG CAA TCA TTC CCG ATT AGG TGG GAG GCT Gln Cys Leu Ala Val Ile Gln Gln Ser Phe Pro Ile Arg Trp Glu Ala 1990 1995 2000	11434
GTT TCA GTA AAA GGA GGA TAC AAG CAG AAG TGG AGT ACT AGA GGT GAT Val Ser Val Lys Gly Gly Tyr Lys Gln Lys Trp Ser Thr Arg Gly Asp 2005 2010 2015	11482
GGG CTC CCA AAA GAT ACC CGA ACT TCA GAC TCC TTG GCC CCA ATC GGG Gly Leu Pro Lys Asp Thr Arg Thr Ser Asp Ser Leu Ala Pro Ile Gly 2020 2025 2030	11530
AAC TGG ATC AGA TCT CTG GAA TTG GTC CGA AAC CAA GTT CGT CTA AAT Asn Trp Ile Arg Ser Leu Glu Leu Val Arg Asn Gln Val Arg Leu Asn 2035 2040 2045 2050	11578
CCA TTC AAT GAG ATC TTG TTC AAT CAG CTA TGT CGT ACA GTG GAT AAT Pro Phe Asn Glu Ile Leu Phe Asn Gln Leu Cys Arg Thr Val Asp Asn 2055 2060 2065	11626
CAT TTG AAA TGG TCA AAT TTG CGA AGA AAC ACA GGA ATG ATT GAA TGG His Leu Lys Trp Ser Asn Leu Arg Arg Asn Thr Gly Met Ile Glu Trp 2070 2075 2080	11674
ATC AAT AGA CGA ATT TCA AAA GAA GAC CGG TCT ATA CTG ATG TTG AAG Ile Asn Arg Arg Ile Ser Lys Glu Asp Arg Ser Ile Leu Met Leu Lys 2085 2090 2095	11722
AGT GAC CTA CAC GAG GAA AAC TCT TGG AGA GAT TAA AAAATCATGA Ser Asp Leu His Glu Glu Asn Ser Trp Arg Asp 2100 2105	11768

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TCCGACCTGG GCATCCGAAG GAGGACGTCG TCCACTCGGA TGGCTAAGGG AGGGGCCCCC 11948
GCGGGGCTGC TAACAAAGCC CGAAAGGAAG CTGAGTTGGC TGCTGCCACC GCTGAGCAAT 12008
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CTCCGGTTCC CAACGATCAA GGCGAGTTAC ATGATCCCCC ATGTTGTGCA AAAAAGCGGT 13748
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GCGCACATTT CCCCAGAAAAG TGC 14311

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Ser Val Thr Val Lys Arg Ile Ile Asp Asn Thr Val Ile Val Pro
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Lys Leu Pro Ala Asn Glu Asp Pro Val Glu Tyr Pro Ala Asp Tyr Phe
 20           25           30
Arg Lys Ser Lys Glu Ile Pro Leu Tyr Ile Asn Thr Thr Lys Ser Leu
 35           40           45
Ser Asp Leu Arg Gly Tyr Val Tyr Gln Gly Leu Lys Ser Gly Asn Val
 50           55           60
Ser Ile Ile His Val Asn Ser Tyr Leu Tyr Gly Ala Leu Lys Asp Ile
 65           70           75           80
Arg Gly Lys Leu Asp Lys Asp Trp Ser Ser Phe Gly Ile Asn Ile Gly
 85           90           95
Lys Ala Gly Asp Thr Ile Gly Ile Phe Asp Leu Val Ser Leu Lys Ala
100           105           110
Leu Asp Gly Val Leu Pro Asp Gly Val Ser Asp Ala Ser Arg Thr Ser
115           120           125
Ala Asp Asp Lys Trp Leu Pro Leu Tyr Leu Leu Gly Leu Tyr Arg Val
130           135           140
Gly Arg Thr Gln Met Pro Glu Tyr Arg Lys Lys Leu Met Asp Gly Leu
145           150           155           160
Thr Asn Gln Cys Lys Met Ile Asn Glu Gln Phe Glu Pro Leu Val Pro
165           170           175
Glu Gly Arg Asp Ile Phe Asp Val Trp Gly Asn Asp Ser Asn Tyr Thr
180           185           190
Lys Ile Val Ala Ala Val Asp Met Phe Phe His Met Phe Lys Lys His

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195 200 205
 Glu Cys Ala Ser Phe Arg Tyr Gly Thr Ile Val Ser Arg Phe Lys Asp
 210 215 220
 Cys Ala Ala Leu Ala Thr Phe Gly His Leu Cys Lys Ile Thr Gly Met
 225 230 235 240
 Ser Thr Glu Asp Val Thr Thr Trp Ile Leu Asn Arg Glu Val Ala Asp
 245 250 255
 Glu Met Val Gln Met Met Leu Pro Gly Gln Glu Ile Asp Lys Ala Asp
 260 265 270
 Ser Tyr Met Pro Tyr Leu Ile Asp Phe Gly Leu Ser Ser Lys Ser Pro
 275 280 285
 Tyr Ser Ser Val Lys Asn Pro Ala Phe His Phe Trp Gly Gln Leu Thr
 290 295 300
 Ala Leu Leu Leu Arg Ser Thr Arg Ala Arg Asn Ala Arg Gln Pro Asp
 305 310 315 320
 Asp Ile Glu Tyr Thr Ser Leu Thr Thr Ala Gly Leu Leu Tyr Ala Tyr
 325 330 335
 Ala Val Gly Ser Ser Ala Asp Leu Ala Gln Gln Phe Cys Val Gly Asp
 340 345 350
 Asn Lys Tyr Thr Pro Asp Asp Ser Thr Gly Gly Leu Thr Thr Asn Ala
 355 360 365
 Pro Pro Gln Gly Arg Asp Val Val Glu Trp Leu Gly Trp Phe Glu Asp
 370 375 380
 Gln Asn Arg Lys Pro Thr Pro Asp Met Met Gln Tyr Ala Lys Arg Ala
 385 390 395 400
 Val Met Ser Leu Gln Gly Leu Arg Glu Lys Thr Ile Gly Lys Tyr Ala
 405 410 415
 Lys Ser Glu Phe Asp Lys
 420

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 265 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Asp Asn Leu Thr Lys Val Arg Glu Tyr Leu Lys Ser Tyr Ser Arg
 1 5 10 15
 Leu Asp Gln Ala Val Gly Glu Ile Asp Glu Ile Glu Ala Gln Arg Ala
 20 25 30
 Glu Lys Ser Asn Tyr Glu Leu Phe Gln Glu Asp Gly Val Glu Glu His
 35 40 45
 Thr Lys Pro Ser Tyr Phe Gln Ala Ala Asp Asp Ser Asp Thr Glu Ser
 50 55 60

Glu Pro Glu Ile Glu Asp Asn Gln Gly Leu Tyr Ala Pro Asp Pro Glu
 65 70 75 80
 Ala Glu Gln Val Glu Gly Phe Ile Gln Gly Pro Leu Asp Asp Tyr Ala
 85 90 95
 Asp Glu Glu Val Asp Val Val Phe Thr Ser Asp Trp Lys Gln Pro Glu
 100 105 110
 Leu Glu Ser Asp Glu His Gly Lys Thr Leu Arg Leu Thr Ser Pro Glu
 115 120 125
 Gly Leu Ser Gly Glu Gln Lys Ser Gln Trp Leu Ser Thr Ile Lys Ala
 130 135 140
 Val Val Gln Ser Ala Lys Tyr Trp Asn Leu Ala Glu Cys Thr Phe Glu
 145 150 155 160
 Ala Ser Gly Glu Gly Val Ile Met Lys Glu Arg Gln Ile Thr Pro Asp
 165 170 175
 Val Tyr Lys Val Thr Pro Val Met Asn Thr His Pro Ser Gln Ser Glu
 180 185 190
 Ala Val Ser Asp Val Trp Ser Leu Ser Lys Thr Ser Met Thr Phe Gln
 195 200 205
 Pro Lys Lys Ala Ser Leu Gln Pro Leu Thr Ile Ser Leu Asp Glu Leu
 210 215 220
 Phe Ser Ser Arg Gly Glu Phe Ile Ser Val Gly Gly Asp Gly Arg Met
 225 230 235 240
 Ser His Lys Glu Ala Ile Leu Leu Gly Leu Arg Tyr Lys Lys Leu Tyr
 245 250 255
 Asn Gln Ala Arg Val Lys Tyr Ser Leu
 260 265

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 229 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ser Ser Leu Lys Lys Ile Leu Gly Leu Lys Gly Lys Lys
 1 5 10 15
 Ser Lys Lys Leu Gly Ile Ala Pro Pro Tyr Glu Glu Asp Thr Ser
 20 25 30
 Met Glu Tyr Ala Pro Ser Ala Pro Ile Asp Lys Ser Tyr Phe Gly Val
 35 40 45
 Asp Glu Met Asp Thr Tyr Asp Pro Asn Gln Leu Arg Tyr Glu Lys Phe
 50 55 60
 Phe Phe Thr Val Lys Met Thr Val Arg Ser Asn Arg Pro Phe Arg Thr
 65 70 75 80
 Tyr Ser Asp Val Ala Ala Ala Val Ser His Trp Asp His Met Tyr Ile

85 90 95

Gly Met Ala Gly Lys Arg Pro Phe Tyr Lys Ile Leu Ala Phe Leu Gly
100 105 110

Ser Ser Asn Leu Lys Ala Thr Pro Ala Val Leu Ala Asp Gln Gly Gln
115 120 125

Pro Glu Tyr His Thr His Cys Glu Gly Arg Ala Tyr Leu Pro His Arg
130 135 140

Met Gly Lys Thr Pro Pro Met Leu Asn Val Pro Glu His Phe Arg Arg
145 150 155 160

Pro Phe Asn Ile Gly Leu Tyr Lys Gly Thr Ile Glu Leu Thr Met Thr
165 170 175

Ile Tyr Asp Asp Glu Ser Leu Glu Ala Ala Pro Met Ile Trp Asp His
180 185 190

Phe Asn Ser Ser Lys Phe Ser Asp Phe Arg Glu Lys Ala Leu Met Phe
195 200 205

Gly Leu Ile Val Glu Lys Lys Ala Ser Gly Ala Trp Val Leu Asp Ser
210 215 220

Ile Ser His Phe Lys
225

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 511 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Lys Cys Leu Leu Tyr Leu Ala Phe Leu Phe Ile Gly Val Asn Cys
1 5 10 15

Lys Phe Thr Ile Val Phe Pro His Asn Gln Lys Gly Asn Trp Lys Asn
20 25 30

Val Pro Ser Asn Tyr His Tyr Cys Pro Ser Ser Ser Asp Leu Asn Trp
35 40 45

His Asn Asp Leu Ile Gly Thr Ala Ile Gln Val Lys Met Pro Lys Ser
50 55 60

His Lys Ala Ile Gln Ala Asp Gly Trp Met Cys His Ala Ser Lys Trp
65 70 75 80

Val Thr Thr Cys Asp Phe Arg Trp Tyr Gly Pro Lys Tyr Ile Thr Gln
85 90 95

Ser Ile Arg Ser Phe Thr Pro Ser Val Glu Gln Cys Lys Glu Ser Ile
100 105 110

Glu Gln Thr Lys Gln Gly Thr Trp Leu Asn Pro Gly Phe Pro Pro Gln
115 120 125

Ser Cys Gly Tyr Ala Thr Val Thr Asp Ala Glu Ala Val Ile Val Gln
130 135 140

Val Thr Pro His His Val Leu Val Asp Glu Tyr Thr Gly Glu Trp Val
 145 150 155 160
 Asp Ser Gln Phe Ile Asn Gly Lys Cys Ser Asn Tyr Ile Cys Pro Thr
 165 170 175
 Val His Asn Ser Thr Thr Trp His Ser Asp Tyr Lys Val Lys Gly Leu
 180 185 190
 Cys Asp Ser Asn Leu Ile Ser Met Asp Ile Thr Phe Phe Ser Glu Asp
 195 200 205
 Gly Glu Leu Ser Ser Leu Gly Lys Glu Gly Thr Gly Phe Arg Ser Asn
 210 215 220
 Tyr Phe Ala Tyr Glu Thr Gly Gly Lys Ala Cys Lys Met Gln Tyr Cys
 225 230 235 240
 Lys His Trp Gly Val Arg Leu Pro Ser Gly Val Trp Phe Glu Met Ala
 245 250 255
 Asp Lys Asp Leu Phe Ala Ala Ala Arg Phe Pro Glu Cys Pro Glu Gly
 260 265 270
 Ser Ser Ile Ser Ala Pro Ser Gln Thr Ser Val Asp Val Ser Leu Ile
 275 280 285
 Gln Asp Val Glu Arg Ile Leu Asp Tyr Ser Leu Cys Gln Glu Thr Trp
 290 295 300
 Ser Lys Ile Arg Ala Gly Leu Pro Ile Ser Pro Val Asp Leu Ser Tyr
 305 310 315 320
 Leu Ala Pro Lys Asn Pro Gly Thr Gly Pro Ala Phe Thr Ile Ile Asn
 325 330 335
 Gly Thr Leu Lys Tyr Phe Glu Thr Arg Tyr Ile Arg Val Asp Ile Ala
 340 345 350
 Ala Pro Ile Leu Ser Arg Met Val Gly Met Ile Ser Gly Thr Thr Thr
 355 360 365
 Glu Arg Glu Leu Trp Asp Asp Trp Ala Pro Tyr Glu Asp Val Glu Ile
 370 375 380
 Gly Pro Asn Gly Val Leu Arg Thr Ser Ser Gly Tyr Lys Phe Pro Leu
 385 390 395 400
 Tyr Met Ile Gly His Gly Met Leu Asp Ser Asp Leu His Leu Ser Ser
 405 410 415
 Lys Ala Gln Val Phe Glu His Pro His Ile Gln Asp Ala Ala Ser Gln
 420 425 430
 Leu Pro Asp Asp Glu Ser Leu Phe Phe Gly Asp Thr Gly Leu Ser Lys
 435 440 445
 Asn Pro Ile Glu Leu Val Glu Gly Trp Phe Ser Ser Trp Lys Ser Ser
 450 455 460
 Ile Ala Ser Phe Phe Phe Ile Ile Gly Leu Ile Ile Gly Leu Phe Leu
 465 470 475 480
 Val Leu Arg Val Gly Ile His Leu Cys Ile Lys Leu Lys His Thr Lys
 485 490 495
 Lys Arg Gln Ile Tyr Thr Asp Ile Glu Met Asn Arg Leu Gly Lys

500

505

510

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2109 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Glu Val His Asp Phe Glu Thr Asp Glu Phe Asn Asp Phe Asn Glu
 1 5 10 15
 Asp Asp Tyr Ala Thr Arg Glu Phe Leu Asn Pro Asp Glu Arg Met Thr
 20 25 30
 Tyr Leu Asn His Ala Asp Tyr Asn Leu Asn Ser Pro Leu Ile Ser Asp
 35 40 45
 Asp Ile Asp Asn Leu Ile Arg Lys Phe Asn Ser Leu Pro Ile Pro Ser
 50 55 60
 Met Trp Asp Ser Lys Asn Trp Asp Gly Val Leu Glu Met Leu Thr Ser
 65 70 75 80
 Cys Gln Ala Asn Pro Ile Ser Thr Ser Gln Met His Lys Trp Met Gly
 85 90 95
 Ser Trp Leu Met Ser Asp Asn His Asp Ala Ser Gln Gly Tyr Ser Phe
 100 105 110
 Leu His Glu Val Asp Lys Glu Ala Glu Ile Thr Phe Asp Val Val Glu
 115 120 125
 Thr Phe Ile Arg Gly Trp Gly Asn Lys Pro Ile Glu Tyr Ile Lys Lys
 130 135 140
 Glu Arg Trp Thr Asp Ser Phe Lys Ile Leu Ala Tyr Leu Cys Gln Lys
 145 150 155 160
 Phe Leu Asp Leu His Lys Leu Thr Leu Ile Leu Asn Ala Val Ser Glu
 165 170 175
 Val Glu Leu Leu Asn Leu Ala Arg Thr Phe Lys Gly Lys Val Arg Arg
 180 185 190
 Ser Ser His Gly Thr Asn Ile Cys Arg Ile Arg Val Pro Ser Leu Gly
 195 200 205
 Pro Thr Phe Ile Ser Glu Gly Trp Ala Tyr Phe Lys Lys Leu Asp Ile
 210 215 220
 Leu Met Asp Arg Asn Phe Leu Leu Met Val Lys Asp Val Ile Ile Gly
 225 230 235 240
 Arg Met Gln Thr Val Leu Ser Met Val Cys Arg Ile Asp Asn Leu Phe
 245 250 255
 Ser Glu Gln Asp Ile Phe Ser Leu Leu Asn Ile Tyr Arg Ile Gly Asp
 260 265 270
 Lys Ile Val Glu Arg Gln Gly Asn Phe Ser Tyr Asp Leu Ile Lys Met

275 280 285
 Val Glu Pro Ile Cys Asn Leu Lys Leu Met Lys Leu Ala Arg Glu Ser
 290 295 300
 Arg Pro Leu Val Pro Gln Phe Pro His Phe Glu Asn His Ile Lys Thr
 305 310 315 320
 Ser Val Asp Glu Gly Ala Lys Ile Asp Arg Gly Ile Arg Phe Leu His
 325 330 335
 Asp Gln Ile Met Ser Val Lys Thr Val Asp Leu Thr Leu Val Ile Tyr
 340 345 350
 Gly Ser Phe Arg His Trp Gly His Pro Phe Ile Asp Tyr Tyr Thr Gly
 355 360 365
 Leu Glu Lys Leu His Ser Gln Val Thr Met Lys Lys Asp Ile Asp Val
 370 375 380
 Ser Tyr Ala Lys Ala Leu Ala Ser Asp Leu Ala Arg Ile Val Leu Phe
 385 390 395 400
 Gln Gln Phe Asn Asp His Lys Lys Trp Phe Val Asn Gly Asp Leu Leu
 405 410 415
 Pro His Asp His Pro Phe Lys Ser His Val Lys Glu Asn Thr Trp Pro
 420 425 430
 Thr Ala Ala Gln Val Gln Asp Phe Gly Asp Lys Trp His Glu Leu Pro
 435 440 445
 Leu Ile Lys Cys Phe Glu Ile Pro Asp Leu Leu Asp Pro Ser Ile Ile
 450 455 460
 Tyr Ser Asp Lys Ser His Ser Met Asn Arg Ser Glu Val Leu Lys His
 465 470 475 480
 Val Arg Met Asn Pro Asn Thr Pro Ile Pro Ser Lys Lys Val Leu Gln
 485 490 495
 Thr Met Leu Asp Thr Lys Ala Thr Asn Trp Lys Glu Phe Leu Lys Glu
 500 505 510
 Ile Asp Glu Lys Gly Leu Asp Asp Asp Asp Leu Ile Ile Gly Leu Lys
 515 520 525
 Gly Lys Glu Arg Glu Leu Lys Leu Ala Gly Arg Phe Phe Ser Leu Met
 530 535 540
 Ser Trp Lys Leu Arg Glu Tyr Phe Val Ile Thr Glu Tyr Leu Ile Lys
 545 550 555 560
 Thr His Phe Val Pro Met Phe Lys Gly Leu Thr Met Ala Asp Asp Leu
 565 570 575
 Thr Ala Val Ile Lys Lys Met Leu Asp Ser Ser Ser Gly Gln Gly Leu
 580 585 590
 Lys Ser Tyr Glu Ala Ile Cys Ile Ala Asn His Ile Asp Tyr Glu Lys
 595 600 605
 Trp Asn Asn His Gln Arg Lys Leu Ser Asn Gly Pro Val Phe Arg Val
 610 615 620
 Met Gly Gln Phe Leu Gly Tyr Pro Ser Leu Ile Glu Arg Thr His Glu
 625 630 635 640

Phe Phe Glu Lys Ser Leu Ile Tyr Tyr Asn Gly Arg Pro Asp Leu Met
 645 650 655
 Arg Val His Asn Asn Thr Leu Ile Asn Ser Thr Ser Gln Arg Val Cys
 660 665 670
 Trp Gln Gly Gln Glu Gly Gly Leu Glu Gly Leu Arg Gln Lys Gly Trp
 675 680 685
 Thr Ile Leu Asn Leu Leu Val Ile Gln Arg Glu Ala Lys Ile Arg Asn
 690 695 700
 Thr Ala Val Lys Val Leu Ala Gln Gly Asp Asn Gln Val Ile Cys Thr
 705 710 715 720
 Gln Tyr Lys Thr Lys Lys Ser Arg Asn Val Val Glu Leu Gln Gly Ala
 725 730 735
 Leu Asn Gln Met Val Ser Asn Asn Glu Lys Ile Met Thr Ala Ile Lys
 740 745 750
 Ile Gly Thr Gly Lys Leu Gly Leu Leu Ile Asn Asp Asp Glu Thr Met
 755 760 765
 Gln Ser Ala Asp Tyr Leu Asn Tyr Gly Lys Ile Pro Ile Phe Arg Gly
 770 775 780
 Val Ile Arg Gly Leu Glu Thr Lys Arg Trp Ser Arg Val Thr Cys Val
 785 790 795 800
 Thr Asn Asp Gln Ile Pro Thr Cys Ala Asn Ile Met Ser Ser Val Ser
 805 810 815
 Thr Asn Ala Leu Thr Val Ala His Phe Ala Glu Asn Pro Ile Asn Ala
 820 825 830
 Met Ile Gln Tyr Asn Tyr Phe Gly Thr Phe Ala Arg Leu Leu Leu Met
 835 840 845
 Met His Asp Pro Ala Leu Arg Gln Ser Leu Tyr Glu Val Gln Asp Lys
 850 855 860
 Ile Pro Gly Leu His Ser Ser Thr Phe Lys Tyr Ala Met Leu Tyr Leu
 865 870 875 880
 Asp Pro Ser Ile Gly Gly Val Ser Gly Met Ser Leu Ser Arg Phe Leu
 885 890 895
 Ile Arg Ala Phe Pro Asp Pro Val Thr Glu Ser Leu Ser Phe Trp Arg
 900 905 910
 Phe Ile His Val His Ala Arg Ser Glu His Leu Lys Glu Met Ser Ala
 915 920 925
 Val Phe Gly Asn Pro Glu Ile Ala Lys Phe Arg Ile Thr His Ile Asp
 930 935 940
 Lys Leu Val Glu Asp Pro Thr Ser Leu Asn Ile Ala Met Gly Met Ser
 945 950 955 960
 Pro Ala Asn Leu Leu Lys Thr Glu Val Lys Lys Cys Leu Ile Glu Ser
 965 970 975
 Arg Gln Thr Ile Arg Asn Gln Val Ile Lys Asp Ala Thr Ile Tyr Leu
 980 985 990
 Tyr His Glu Glu Asp Arg Leu Arg Ser Phe Leu Trp Ser Ile Asn Pro

995	1000	1005
Leu Phe Pro Arg Phe Leu Ser Glu Phe Lys Ser Gly Thr Phe Leu Gly 1010 1015 1020		
Val Ala Asp Gly Leu Ile Ser Leu Phe Gln Asn Ser Arg Thr Ile Arg 1025 1030 1035 1040		
Asn Ser Phe Lys Lys Lys Tyr His Arg Glu Leu Asp Asp Leu Ile Val 1045 1050 1055		
Arg Ser Glu Val Ser Ser Leu Thr His Leu Gly Lys Leu His Leu Arg 1060 1065 1070		
Arg Gly Ser Cys Lys Met Trp Thr Cys Ser Ala Thr His Ala Asp Thr 1075 1080 1085		
Leu Arg Tyr Lys Ser Trp Gly Arg Thr Val Ile Gly Thr Thr Val Pro 1090 1095 1100		
His Pro Leu Glu Met Leu Gly Pro Gln His Arg Lys Glu Thr Pro Cys 1105 1110 1115 1120		
Ala Pro Cys Asn Thr Ser Gly Phe Asn Tyr Val Ser Val His Cys Pro 1125 1130 1135		
Asp Gly Ile His Asp Val Phe Ser Ser Arg Gly Pro Leu Pro Ala Tyr 1140 1145 1150		
Leu Gly Ser Lys Thr Ser Glu Ser Thr Ser Ile Leu Gln Pro Trp Glu 1155 1160 1165		
Arg Glu Ser Lys Val Pro Leu Ile Lys Arg Ala Thr Arg Leu Arg Asp 1170 1175 1180		
Ala Ile Ser Trp Phe Val Glu Pro Asp Ser Lys Leu Ala Met Thr Ile 1185 1190 1195 1200		
Leu Ser Asn Ile His Ser Leu Thr Gly Glu Glu Trp Thr Lys Arg Gln 1205 1210 1215		
His Gly Phe Lys Arg Thr Gly Ser Ala Leu His Arg Phe Ser Thr Ser 1220 1225 1230		
Arg Met Ser His Gly Gly Phe Ala Ser Gln Ser Thr Ala Ala Leu Thr 1235 1240 1245		
Arg Leu Met Ala Thr Thr Asp Thr Met Arg Asp Leu Gly Asp Gln Asn 1250 1255 1260		
Phe Asp Phe Leu Phe Gln Ala Thr Leu Leu Tyr Ala Gln Ile Thr Thr 1265 1270 1275 1280		
Thr Val Ala Arg Asp Gly Trp Ile Thr Ser Cys Thr Asp His Tyr His 1285 1290 1295		
Ile Ala Cys Lys Ser Cys Leu Arg Pro Ile Glu Glu Ile Thr Leu Asp 1300 1305 1310		
Ser Ser Met Asp Tyr Thr Pro Pro Asp Val Ser His Val Leu Lys Thr 1315 1320 1325		
Trp Arg Asn Gly Glu Gly Ser Trp Gly Gln Glu Ile Lys Gln Ile Tyr 1330 1335 1340		
Pro Leu Glu Gly Asn Trp Lys Asn Leu Ala Pro Ala Glu Gln Ser Tyr 1345 1350 1355 1360		

Gln Val Gly Arg Cys Ile Gly Phe Leu Tyr Gly Asp Leu Ala Tyr Arg
 1365 1370 1375
 Lys Ser Thr His Ala Glu Asp Ser Ser Leu Phe Pro Leu Ser Ile Gln
 1380 1385 1390
 Gly Arg Ile Arg Gly Arg Gly Phe Leu Lys Gly Leu Leu Asp Gly Leu
 1395 1400 1405
 Met Arg Ala Ser Cys Cys Gln Val Ile His Arg Arg Ser Leu Ala His
 1410 1415 1420
 Leu Lys Arg Pro Ala Asn Ala Val Tyr Gly Gly Leu Ile Tyr Leu Ile
 1425 1430 1435 1440
 Asp Lys Leu Ser Val Ser Pro Pro Phe Leu Ser Leu Thr Arg Ser Gly
 1445 1450 1455
 Pro Ile Arg Asp Glu Leu Glu Thr Ile Pro His Lys Ile Pro Thr Ser
 1460 1465 1470
 Tyr Pro Thr Ser Asn Arg Asp Met Gly Val Ile Val Arg Asn Tyr Phe
 1475 1480 1485
 Lys Tyr Gln Cys Arg Leu Ile Glu Lys Gly Lys Tyr Arg Ser His Tyr
 1490 1495 1500
 Ser Gln Leu Trp Leu Phe Ser Asp Val Leu Ser Ile Asp Phe Ile Gly
 1505 1510 1515 1520
 Pro Phe Ser Ile Ser Thr Thr Leu Leu Gln Ile Leu Tyr Lys Pro Phe
 1525 1530 1535
 Leu Ser Gly Lys Asp Lys Asn Glu Leu Arg Glu Leu Ala Asn Leu Ser
 1540 1545 1550
 Ser Leu Leu Arg Ser Gly Glu Gly Trp Glu Asp Ile His Val Lys Phe
 1555 1560 1565
 Phe Thr Lys Asp Ile Leu Leu Cys Pro Glu Glu Ile Arg His Ala Cys
 1570 1575 1580
 Lys Phe Gly Ile Ala Lys Asp Asn Asn Lys Asp Met Ser Tyr Pro Pro
 1585 1590 1595 1600
 Trp Gly Arg Glu Ser Arg Gly Thr Ile Thr Thr Ile Pro Val Tyr Tyr
 1605 1610 1615
 Thr Thr Thr Pro Tyr Pro Lys Met Leu Glu Met Pro Pro Arg Ile Gln
 1620 1625 1630
 Asn Pro Leu Leu Ser Gly Ile Arg Leu Gly Gln Leu Pro Thr Gly Ala
 1635 1640 1645
 His Tyr Lys Ile Arg Ser Ile Leu His Gly Met Gly Ile His Tyr Arg
 1650 1655 1660
 Asp Phe Leu Ser Cys Gly Asp Gly Ser Gly Gly Met Thr Ala Ala Leu
 1665 1670 1675 1680
 Leu Arg Glu Asn Val His Ser Arg Gly Ile Phe Asn Ser Leu Leu Glu
 1685 1690 1695
 Leu Ser Gly Ser Val Met Arg Gly Ala Ser Pro Glu Pro Pro Ser Ala
 1700 1705 1710
 Leu Glu Thr Leu Gly Gly Asp Lys Ser Arg Cys Val Asn Gly Glu Thr

1715	1720	1725
Cys Trp Glu Tyr Pro Ser Asp Leu Cys Asp Pro Arg Thr Trp Asp Tyr		
1730	1735	1740
Phe Leu Arg Leu Lys Ala Gly Leu Gly Leu Gln Ile Asp Leu Ile Val		
1745	1750	1755 1760
Met Asp Met Glu Val Arg Asp Ser Ser Thr Ser Leu Lys Ile Glu Thr		
	1765	1770 1775
Asn Val Arg Asn Tyr Val His Arg Ile Leu Asp Glu Gln Gly Val Leu		
	1780	1785 1790
Ile Tyr Lys Thr Tyr Gly Thr Tyr Ile Cys Glu Ser Glu Lys Asn Ala		
	1795	1800 1805
Val Thr Ile Leu Gly Pro Met Phe Lys Thr Val Asp Leu Val Gln Thr		
	1810	1815 1820
Glu Phe Ser Ser Ser Gln Thr Ser Glu Val Tyr Met Val Cys Lys Gly		
	1825	1830 1835 1840
Leu Lys Lys Leu Ile Asp Glu Pro Asn Pro Asp Trp Ser Ser Ile Asn		
	1845	1850 1855
Glu Ser Trp Lys Asn Leu Tyr Ala Phe Gln Ser Ser Glu Gln Glu Phe		
	1860	1865 1870
Ala Arg Ala Lys Lys Val Ser Thr Tyr Phe Thr Leu Thr Gly Ile Pro		
	1875	1880 1885
Ser Gln Phe Ile Pro Asp Pro Phe Val Asn Ile Glu Thr Met Leu Gln		
	1890	1895 1900
Ile Phe Gly Val Pro Thr Gly Val Ser His Ala Ala Ala Leu Lys Ser		
	1905	1910 1915 1920
Ser Asp Arg Pro Ala Asp Leu Leu Thr Ile Ser Leu Phe Tyr Met Ala		
	1925	1930 1935
Ile Ile Ser Tyr Tyr Asn Ile Asn His Ile Arg Val Gly Pro Ile Pro		
	1940	1945 1950
Pro Asn Pro Pro Ser Asp Gly Ile Ala Gln Asn Val Gly Ile Ala Ile		
	1955	1960 1965
Thr Gly Ile Ser Phe Trp Leu Ser Leu Met Glu Lys Asp Ile Pro Leu		
	1970	1975 1980
Tyr Gln Gln Cys Leu Ala Val Ile Gln Gln Ser Phe Pro Ile Arg Trp		
	1985	1990 1995 2000
Glu Ala Val Ser Val Lys Gly Gly Tyr Lys Gln Lys Trp Ser Thr Arg		
	2005	2010 2015
Gly Asp Gly Leu Pro Lys Asp Thr Arg Thr Ser Asp Ser Leu Ala Pro		
	2020	2025 2030
Ile Gly Asn Trp Ile Arg Ser Leu Glu Leu Val Arg Asn Gln Val Arg		
	2035	2040 2045
Leu Asn Pro Phe Asn Glu Ile Leu Phe Asn Gln Leu Cys Arg Thr Val		
	2050	2055 2060
Asp Asn His Leu Lys Trp Ser Asn Leu Arg Arg Asn Thr Gly Met Ile		
	2065	2070 2075 2080

Glu Trp Ile Asn Arg Arg Ile Ser Lys Glu Asp Arg Ser Ile Leu Met
 2085 2090 2095

Leu Lys Ser Asp Leu His Glu Glu Asn Ser Trp Arg Asp
 2100 2105

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14311 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

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GCACTTTTCG GGGAAATGTG CGCGGAACCC CTATTTGTTT ATTTTCTAA ATACATTCAA      60
ATATGTATCC GTCATGAGA CAATAACCCT GATAAATGCT TCAATAATAT TGAAAAAGGA      120
AGAGTATGAG TATTCACAT TTCCGTGTCG CCCTTATTCC CTTTTTTGCG GCATTTTGCC      180
TTCCTGTTTT TGCTCACCCA GAAACGCTGG TGAAAGTAAA AGATGCTGAA GATCAGTTGG      240
GTGCACGAGT GGGTTACATC GAACTGGATC TCAACAGCGG TAAGATCCTT GAGAGTTTTT      300
GCCCCGAAGA ACGTTTTCCA ATGATGAGCA CTTTTAAAGT TCTGCTATGT GGCGCGGTAT      360
TATCCCGTAT TGACGCCGGG CAAGAGCAAC TCGGTCGCCG CATACACTAT TCGCGAATG      420
ACTTGGTTGA GTACTACCA GTCACAGAAA AGCATCTTAC GGATGGCATG ACAGTAAGAG      480
AATTATGCAG TGCTGCCATA ACCATGAGTG ATAACACTGC GGCCAACTTA CTTCTGACAA      540
CGATCGGAGG ACCGAAGGAG CTAACCGCTT TTTTGCACAA CATGGGGGAT CATGTAAGTC      600
GCCTTGATCG TTGGGAACCG GAGCTGAATG AAGCCATACC AAACGACGAG CGTGACACCA      660
CGATGCCTGT AGCAATGGCA ACAACGTTGC GCAAACCTATT AACTGGCGAA CTACTTACTC      720
TAGCTTCCCG GCAACAATTA ATAGACTGGA TGGAGGCGGA TAAAGTTGCA GGACCACTTC      780
TGCGCTCGGC CCTTCCGGCT GGCTGGTTTA TTGCTGATAA ATCTGGAGCC GGTGAGCGTG      840
GGTCTCGCGG TATCATTGCA GCACTGGGGC CAGATGGTAA GCCCTCCCGT ATCGTAGTTA      900
TCTACACGAC GGGGAGTCAG GCAACTATGG ATGAACGAAA TAGACAGATC GCTGAGATAG      960
GTGCCTCACT GATTAAGCAT TGGTAACTGT CAGACCAAGT TTAATCATAT AACTTTTAGA     1020
TTGATTTAAA ACTTCATTTT TAATTTAAAA GGATCTAGGT GAAGATCCTT TTTGATAATC     1080
TCATGACCAA AATCCCTTAA CGTGAGTTTT CGTTCCACTG AGCGTCAGAC CCCGTAGAAA     1140
AGATCAAAGG ATCTTCTTGA GATCCTTTTT TTCTGCGCGT AATCTGCTGC TTGCAAACAA     1200
AAAAACCACC GCTACCAGCG GTGGTTTGTT TGCCGGATCA AGAGCTACCA ACTCTTTTTC     1260
CGAAGGTAAC TGGCTTCAGC AGAGCGCAGA TACCAAATAC TGTCTTCTA GTGTAGCCGT     1320
AGTTAGGCCA CCACTTCAAG AACTCTGTAG CACCGCCTAC ATACCTCGCT CTGCTAATCC     1380

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TGTTACCACT GGCTGCTGCC AGTGGCGATA AGTCGTGTCT TACCGGGTTG GACTCAAGAC 1440
GATAGTTACC GGATAAGGCG CAGCGGTCGG GCTGAACGGG GGGTTCGTGC ACACAGCCCA 1500
GCTTGGAGCG AACGACCTAC ACCGAACTGA GATACCTACA GCGTGAGCTA TGAGAAAGCG 1560
CCACGCTTCC CGAAGGGAGA AAGGCGGACA GGTATCCGGT AAGCGGCAGG GTCGGAACAG 1620
GAGAGCGCAC GAGGGAGCTT CCAGGGGGAA ACGCCTGGTA TCTTTATAGT CCTGTCGGGT 1680
TTCGCCACCT CTGACTTGAG CGTCGATTTT TGTGATGCTC GTCAGGGGGG CGGAGCCTAT 1740
GGAAAAACGC CAGCAACGCG GCCTTTTTTAC GGTTCCTGGC CTTTTGCTGG CCTTTTGCTC 1800
ACATGTTCTT TCCTGCGTTA TCCCCTGATT CTGTGGATAA CCGTATTACC GCCTTTGAGT 1860
GAGCTGATAC CGCTCGCCGC AGCCGAACGA CCGAGCGCAG CGAGTCAGTG AGCGAGGAAG 1920
CGGAAGAGCG CCCAATACGC AAACCGCCTC TCCCCGCGCG TTGGCCGATT CATTAATGCA 1980
GCTGGCACGA CAGGTTTCCC GACTGGAAAG CGGGCAGTGA GCGCAACGCA ATTAATGTGA 2040
GTTAGCTCAC TCATTAGGCA CCCAGGCTT TACACTTTAT GCTTCCGGCT CGTATGTTGT 2100
GTGGAATTGT GAGCGGATAA CAATTTTACA CAGGAAACAG CTATGACCAT GATTACGCCA 2160
AGCTCGAAAT TAACCCTCAC TAAAGGGAAC AAAAGCTGGA GCTCCACCGC ACTAGTATCG 2220
AGGTCTCGAT CCGGATATAG TTCCTCCTTT CAGCAAAAAA CCCCTCAAGA CCCGTTTAGA 2280
GGCCCCAAGG GGTATGCTA GTTATTGCTC AGCGGTGGCA GCAGCCAACT CAGCTTCCTT 2340
TCGGGCTTTG TTAGCAGCCC CGCGGGGGCC CCTCCCTTAG CCATCCGAGT GGACGACGTC 2400
CTCCTTCGGA TGCCAGGTC GGACCGCGAG GAGGTGGAGA TGCCATGCCG ACCCAAGGAG 2460
ACCACAAAAC CAGATAAAAA ATAAAAACCA CAAGAGGGTC TTAAGGATCA AAGTTTTTTT 2520
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TAGGTCACTC TTCAACATCA GTATAGACCG GTCTTCTTTT GAAATTCGTC TATTGATCCA 2640
TTCAATCATT CCTGTGTTT TTCGCAAATT TGACCATTTC AAATGATTAT CCACTGTACG 2700
ACATAGCTGA TTGAACAAGA TCTCATTGAA TGGATTTAGA CGAACTTGGT TTCGGACCAA 2760
TTCCAGAGAT CTGATCCAGT TCCCGATTGG GGCCAAGGAG TCTGAAGTTC GGGTATCTTT 2820
TGGGAGCCCA TCACCTCTAG TACTCCACTT CTGCTTGTAT CCTCCTTTTA CTGAAACAGC 2880
CTCCACCTA ATCGGGAATG ATTGCTGGAT AACTGCTAAA CACTGTTGAT ATAGTGGAAT 2940
GTCTTTCTCC ATCAAACCTCA GCCAAAAGCT TATACCAGTT ATAGCGATCC CCACATTTTG 3000
TGCAATTCCA TCTGATGGGG GGTTCGGAGG TATCGGTCCT ACTCTGATAT GATTGATGTT 3060
ATAATACGAT ATAATCGCCA TATAAAAAAG GCTAATGGTC AATAAATCTG CAGGTCTATC 3120
AGATGATTTT AAGGCAGCCG CATGAGACAC ACCCGTGGGT ACTCCGAATA TTTGTAGCAT 3180
AGTCTCAATG TTTACAAAAG GATCAGGAAT GAATTGGGAG GGAATACCTG TCAAGGTAAA 3240
GTATGTACTA ACCTTCTTTG CTCTGGCAAA TTCCTGTTCT GATGACTGGA ATGCGTACAG 3300
GTTTTTCCAG GATTCATTGA TGGAAGACCA ATCGGGATTG GGTTCATCGA TTAATTTCTT 3360
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TAAGTCGACC GTCTTGAACA TGGGACCAAG GATTGTTACT GCATTCTTTT CGCTCTCACA 3480
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ATAATTTCTA ACATTCGTCT CAATTTTCAG GCTAGTAGAA GAATCCCGAA CTTCCATATC 3600
CATTACAATT AAATCAATTT GAAGCCCCAA GCCTGCTTTG AGTCGGAGGA AATAGTCCCA 3660
AGTCCTTGGG TCACATAAGT CAGATGGATA TTCCCAACAT GTTTCACCAT TTACACATCT 3720
CGATTTATCT CCTCCTAAAG TTTCTAGGGC ACTGGGGGGC TCAGGAGAGG CGCCTCGCAT 3780
GACTGACCCT GATAATTCTA ACAGACTATT GAATATTCCT CTGCTATGCA CATTTTCTCG 3840
TAGTAATGCA GCAGTCATCC CTCCGGAGCC GTCTCCACAA CTCAAGAAGT CCCTGTAATG 3900
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AGTGGTGGTA ATTTGAGCAT AGAGCAACGT TGCTTGGAAT AAAAAGTCGA AATTCTGATC 5100
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CAAAAGTCCT AACTTCCCTG TCCCTATTTT GATTGCAGTC ATAATTTTCT CATTATTAGA 6660
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TTTAGCCTCT CTTTGAATAA CCAGTAGATT GAGGATAGTC CATCCTTTTT GCCGTAGACC 6840
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CACAGTTCCC TTTCTGTGGT AGTTCCACTG ATCATTCCGA CCATTCTTGA GAGGATTGGA 9480
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CTCTCAACGT CCTGAATTAG ACTTACATCC ACTGAGGTCT GAGATGGAGC AGAGATACTT	9720
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TTGCCTCCAG TTTTCATAAGC AAAGTAGTTA CTTCTGAACC CTGTGCCCTC CTTTCCCAGG	9900
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 TAACAAAATA TTAACGCTTA CAATTTAGGT G 14311

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TTGTAATACG ACTCACTATA GGG

23

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTGTAATACG ACTCACTATA GGG

23

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ACGAAGACAA ACAAACCATT ATTATCATTA AAAGGCTCAG GAGAACTTT

50

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 136 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGCTGCTAAC AAAGCCCGAA AGGAAGCTGA GTTGGCTGCT GCCACCGCTG AGCAATAACT

60

AGCATAACCC CTTGGGGCCT CTAAACGGGT CTTGAGGGGT TTTTGTCTGA AAGGAGGAAC

120

TATATCCGGA TCGAGA

136

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 83 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGGTCGGCAT GGCATCTCCA CCTCCTCGCG GTCCGACCTG GGCATCCGAA GGAGGACGTC

60

GTCCACTCGG ATGGCTAAGG GAG

83

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 630 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TTGTAGAAGG TTGGTTCAGT AGTTGGAAAA GCTCTATTGC CTCTTTTTTC TTTATCATAG

60

GGTTAATCAT TGGACTATTC TTGGTTCTCC GAGTTGGTAT CCATCTTTGC ATTAAATTAA

120

AGCACACCAA GAAAAGACAG ATTTATACAG ACATAGAGAT GAACCGACTT GGAAAGTAAC

180

TCAAATCCTG CTAGCTATGA AAAAACTAA CAGATATCCA ACCCGGGAGC TAGTTGCGGC	240
CGCCTAGCAG ATTCTTCATG TTTGGACCAA ATCAACTTGT GATACCATGC TCAAAGAGGC	300
CTCAATTATA TTTGAGTTTT TAATTTTTAT GAAAAAACT AACAGCAATC ATGGAAGTCC	360
ACGATTTTGA GACCGACGAG TTCAATGATT TCAATGAAGA TGACTATGCC ACAAGAGAAT	420
TCCTGAATCC CGATGAGCGC ATGACGTACT TGAATCATGC TGATTACAAT TTGAATTCTC	480
CTCTAATTAG TGATGATATT GACAATTGTA TCAGGAAATT CAATTCTCTT CCGATTCCCT	540
CGATGTGGGA TAGTAAGAAC TGGGATGGAG TTCTTGAGAT GTTAACATCA TGTCAAGCCA	600
ATCCCATCTC AACATCTCAG ATGCATAAAT	630

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 630 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATTTATGCAT CTGAGATGTT GAGATGGGAT TGGCTTGACA TGATGTTAAC ATCTCAAGAA	60
CTCCATCCCA GTTCTTACTA TCCCACATCG AGGGAATCGG AAGAGAATTG AATTTCTGA	120
TCAAATTGTC AATATCATCA CTAATTAGAG GAGAATTCAA ATTGTAATCA GCATGATTCA	180
AGTACGTCAT GCGCTCATCG GGATTGAGGA ATTCTCTTGT GGCATAGTCA TCTTCATTGA	240
AATCATTGAA CTCGTCGGTC TCAAAATCGT GGACTTCCAT GATTGCTGTT AGTTTTTTTC	300
ATAAAAATTA AAAACTCAAA TATAATTGAG GCCTCTTTGA GCATGGTATC ACAAGTTGAT	360
TTGGTCCAAA CATGAAGAAT CTGCTAGGCG GCCGCAACTA GCTCCCGGGT TGGATATCTG	420
TTAGTTTTTT TCATAGCTAG CAGGATTGTA GTTACTTTCC AAGTCGGTTC ATCTCTATGT	480
CTGTATAAAT CTGTCTTTTC TTGGTGTGCT TTAATTTAAT GCAAAGATGG ATACCAACTC	540
GGAGAACCAA GAATAGTCCA ATGATTAACC CTATGATAAA GAAAAAAGAG GCAATAGAGC	600
TTTTCCAAC ACTGAACCAA CCTTCTACAA	630

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 11 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: RNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

UCAGGAGAAA C

11

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: RNA

(ix) FEATURE:

- (A) NAME/KEY: 5' Gppp
- (B) LOCATION: 1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AACAGUAAUC

10

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: RNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GAUUACUGUU AAAGUUUCUC CUGA

24

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: RNA

(ix) FEATURE:

- (A) NAME/KEY: polyA
- (B) LOCATION: 10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GCUACAU AUG

10

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: RNA

- (ix) FEATURE:
 (A) NAME/KEY: 5' Gppp
 (B) LOCATION: 1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:
AACAGAUUUC

10

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: RNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:
GAUAUCUGUU AGUUUUUUUC AUAUGUAGC

29

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: RNA

- (ix) FEATURE:
 (A) NAME/KEY: polyA
 (B) LOCATION: 10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:
GUAGACUAUG

10

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: RNA

- (ix) FEATURE:
 (A) NAME/KEY: 5' Gppp
 (B) LOCATION: 1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:
AACAGAUUUC

10

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: RNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GAUAUCUGUU ACUUUUUUUC AUAGUCUAC

29

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: RNA

(ix) FEATURE:

- (A) NAME/KEY: polyA
- (B) LOCATION: 10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

UAUCCCUAUG

10

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: RNA

(ix) FEATURE:

- (A) NAME/KEY: 5' Gppp
- (B) LOCATION: 1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AACAGAGAU

10

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: RNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:
GAUCUCUGUU AGUUUUUUC AUAGGGAUA

29

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA

(ix) FEATURE:
(A) NAME/KEY: polyA
(B) LOCATION: 10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:
AAUUUUUAUG

10

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA

(ix) FEATURE:
(A) NAME/KEY: 5' Gppp
(B) LOCATION: 1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:
AACAGCAAUC

10

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: RNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:
GAUUGCUGUU AGUUUUUUC AUAAAAAUU

29

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: RNA

(ix) FEATURE:

(A) NAME/KEY: polyA

(B) LOCATION: 10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

UUUAAGUAUG

10

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: RNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

AGGAUCAAAG UUUUUUUCAU ACUAAAA

27

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CATTCAAGAC GCTGCTTCGC AACTTCC

27

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CATGAATGTT AACATCTCAA GA

22

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA

- (ix) FEATURE:
 - (A) NAME/KEY: miscellaneous feature
 - (B) LOCATION: 11..12
 - (D) OTHER INFORMATION: Intergenic dinucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GAUNNCUGUU ANUUUUUUUC AUA

23

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: RNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

UAUGAAA AAA A

11

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: RNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

UUUUUUUCAU A

11

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

TATGAAAAA A

11

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CCGGCTCGAG TTGTAATACG ACTCACTATA GGGACGAAGA CAAACAAACC ATTATTATC

59

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GAACTCTCCT CTAGATGAGA AC

22

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 58 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

AGGTCGGACC GCGAGGAGGT GGAGATGCCA TGCCGACCCA CGAAGACCAC AAAACCAG

58

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

WO 96/34625

PCT/US96/06053

ATGTTGAAGA GTGACCTACA CG

22

WHAT IS CLAIMED IS:

1. A recombinant replicable vesiculovirus, the genome of which comprises a foreign RNA sequence.
5
2. The vesiculovirus of claim 1 in which an RNA sequence complementary to said foreign RNA sequence encodes a peptide or protein that is expressed in a suitable host infected by the virus.
10
3. The vesiculovirus of claim 1 in which the peptide or protein is antigenic or immunogenic.
4. The vesiculovirus of claim 2 in which the
15 peptide or protein displays the antigenicity or immunogenicity of an antigen of a pathogenic microorganism.
5. The vesiculovirus of claim 4 in which the pathogenic microorganism is a virus.
20
6. The vesiculovirus of claim 4 in which the pathogenic microorganism is a bacterium.
7. The vesiculovirus of claim 4 in which the
25 pathogenic microorganism is a parasite.
8. The vesiculovirus of claim 4 in which the pathogenic microorganism is a human pathogen.
- 30 9. The vesiculovirus of claim 4 in which the pathogenic microorganism is a non-human pathogen.
10. The vesiculovirus of claim 2 in which the peptide or protein displays the antigenicity or
35 immunogenicity of a tumor specific or tumor associated antigen.

11. Plasmid pVSVFL(+), as deposited with the ATCC and assigned accession number 97134.

12. A nucleic acid comprising the DNA sequence of
5 plasmid pVSVFL(+) as depicted in Figure 1 from nucleotide numbers 623-12088 (a portion of SEQ ID NO:1), in which a region nonessential for vesiculovirus replication has been inserted into or replaced by foreign DNA.

10 13. A host cell containing the recombinant vesiculovirus of claim 1.

14. A method of producing a recombinant vesiculovirus comprising culturing a cell containing (a) a
15 recombinant nucleic acid that can be transcribed to produce an RNA molecule comprising a vesiculovirus antigenomic (+) RNA, in which a region of the RNA nonessential for replication of the vesiculovirus has been inserted into or
replaced by a foreign RNA sequence; (b) a second recombinant
20 nucleic acid encoding a vesiculovirus N protein; (c) a third recombinant nucleic acid encoding a vesiculovirus L protein; and (d) a fourth recombinant nucleic acid encoding a vesiculovirus P protein; whereby the first recombinant nucleic acid is transcribed in the cell to produce said RNA
25 molecule, and the N, L and P proteins are expressed in the cell, and a recombinant replicable vesiculovirus is produced that has a genome that is the complement of said antigenomic RNA comprising said foreign RNA sequence.

30 15. The method according to claim 14 in which the cell is a mammalian cell.

16. The method according to claim 14 in which the first recombinant nucleic acid comprises a first promoter
35 sequence which controls the expression of the RNA molecule in the cell; the second recombinant nucleic acid comprises a second promoter sequence which controls the expression of the

N protein in the cell; the third recombinant nucleic acid comprises a third promoter sequence which controls the expression of the P protein in the cell; and the fourth recombinant nucleic acid comprises a fourth promoter sequence
5 which controls the expression of the L protein in the cell.

17. The method according to claim 14 in which said RNA molecule further comprises a ribozyme sequence immediately downstream of said antigenomic (+) RNA, that
10 cleaves at the 3' terminus of the antigenomic (+) RNA.

18. The method according to claim 14 in which the first recombinant nucleic acid is a DNA plasmid vector comprising the following operatively linked components:

- 15 (a) a promoter;
(b) a DNA sequence that can be transcribed under the control of the promoter in the cell to produce said RNA molecule; and
(c) a transcription termination signal.

20

19. The method according to claim 14 or 18 in which the second recombinant nucleic acid is a DNA plasmid vector comprising the following operatively linked components:

- 25 (a) a promoter which controls the expression of the N protein;
(b) a translation initiation signal;
(c) a DNA sequence encoding the N protein; and
30 (d) a transcription termination signal; and

in which the third recombinant nucleic acid is a DNA plasmid vector comprising the following operatively linked components:

- 35 (a) a promoter which controls the expression of the P protein;
(b) a translation initiation signal;

(c) a DNA sequence encoding the P protein;
and
(d) a transcription termination signal; and
and in which the fourth recombinant nucleic acid is a DNA
5 plasmid vector comprising the following operatively linked
components:

- 10 (a) a promoter which controls the expression
of the L protein;
(b) a translation initiation signal;
(c) a DNA sequence encoding the L protein;
and
(d) a transcription termination signal.

20 20. The method according to claim 17 in which the
15 first recombinant nucleic acid is a DNA plasmid vector
comprising the following operatively linked components:

- (a) a promoter;
(b) a DNA sequence that can be transcribed
under the control of the promoter in the
20 cell to produce said RNA molecule; and
(c) a transcription termination signal.

21. The method according to claim 19 in which the
first recombinant nucleic acid, the second recombinant
25 nucleic acid, the third recombinant nucleic acid, and the
fourth recombinant nucleic acid, each further comprises a
selectable marker.

22. The method according to claim 14 in which the
30 second, third and fourth recombinant nucleic acids form part
of a single recombinant nucleic acid.

23. The method according to claim 16 in which the
first, second, third and fourth promoter sequences are RNA
35 polymerase promoter sequences for the same RNA polymerase,
and in which the cell also contains a cytoplasmic source of
said RNA polymerase.

24. The method according to claim 23 in which the cytoplasmic source of said RNA polymerase is a recombinant vaccinia virus expressing said RNA polymerase in the cell.

5 25. A method of producing a recombinant vesiculovirus comprising culturing a mammalian cell containing:

(a) a first DNA plasmid vector comprising the following operatively linked components:

- 10 (i) a bacteriophage RNA polymerase promoter;
(ii) a first DNA sequence that is transcribed in the cell to produce an RNA molecule comprising (A) a vesiculovirus antigenomic (+) RNA in which a region of
15 the RNA nonessential for replication of the vesiculovirus has been inserted into or replaced by a foreign RNA sequence, and (B) a ribozyme sequence immediately downstream of said antigenomic (+) RNA, that cleaves at the 3' terminus of the
20 antigenomic RNA; and
(iii) a transcription termination signal for the RNA polymerase;

(b) a second DNA plasmid vector comprising the
25 following operatively linked components:

- (i) the bacteriophage RNA polymerase promoter;
(ii) a second DNA sequence encoding an N protein of the vesiculovirus; and
30 (iii) a second transcription termination signal for the RNA polymerase;

(c) a third DNA plasmid vector comprising the following operatively linked components:

- (i) the bacteriophage RNA polymerase
35 promoter;
(ii) a third DNA sequence encoding a P protein of the vesiculovirus; and

- (iii) a third transcription termination signal for the RNA polymerase;
- (d) a fourth DNA plasmid vector comprising the following operatively linked components:
- 5 (i) the bacteriophage RNA polymerase promoter;
- (ii) a fourth DNA sequence encoding an L protein of the vesiculovirus; and
- 10 (iii) a fourth transcription termination signal for the RNA polymerase; and
- (e) a recombinant vaccinia virus comprising a sequence encoding the bacteriophage RNA polymerase; whereby in said cell the first DNA sequence is transcribed to produce said RNA molecule, the N, P, and L proteins and the
- 15 bacteriophage RNA polymerase are expressed, and a recombinant replicable vesiculovirus is produced that has a genome that is the complement of said antigenomic RNA comprising said foreign RNA sequence.

20 26. The method according to claim 25 in which the ribozyme sequence is the sequence of the hepatitis delta virus ribozyme, and the bacteriophage RNA polymerase is the T7 RNA polymerase.

25 27. The method according to claim 14 in which the foreign RNA sequence is the complement of a sequence encoding a protein or peptide that is immunogenic or antigenic.

28. The method according to claim 25 in which the

30 foreign RNA sequence is the complement of a sequence encoding a protein or peptide that is immunogenic or antigenic.

29. The method according to claim 27 or 28 in which the protein or peptide displays the antigenicity or

35 immunogenicity of an antigen of a pathogenic microorganism.

30. The method according to claim 27 or 28 in which the protein or peptide displays the antigenicity or immunogenicity of a tumor specific antigen.

5 31. The method according to claim 25 which further comprises before step (a) the step of introducing said first, second, third and fourth plasmid vectors and said recombinant vaccinia virus into said cell.

10 32. A host cell comprising (a) a recombinant nucleic acid that can be transcribed to produce an RNA molecule comprising a vesiculovirus antigenomic (+) RNA, in which a region of the RNA nonessential for replication of the
15 RNA sequence; (b) a second recombinant nucleic acid encoding a vesiculovirus N protein; (c) a third recombinant nucleic acid encoding a vesiculovirus L protein; and (d) a fourth recombinant nucleic acid encoding a vesiculovirus P protein.

20 33. A host cell comprising:
(a) a first DNA plasmid vector comprising the following operatively linked components:
(i) a bacteriophage RNA polymerase promoter;
25 (ii) a first DNA sequence that is transcribed in the cell to produce an RNA molecule comprising (A) a vesiculovirus antigenomic (+) RNA in which a region of the RNA nonessential for replication of the vesiculovirus has been inserted into
30 or replaced by a foreign RNA sequence, and (B) a ribozyme sequence immediately downstream of said antigenomic (+) RNA, that cleaves at the 3' terminus of the antigenomic RNA; and
35 (iii) a transcription termination signal for the RNA polymerase;

(b) a second DNA plasmid vector comprising the following operatively linked components:

- (i) the bacteriophage RNA polymerase promoter;
- 5 (ii) a second DNA sequence encoding an N protein of the vesiculovirus; and
- (iii) a second transcription termination signal for the RNA polymerase;

(c) a third DNA plasmid vector comprising the following operatively linked components:

- (i) the bacteriophage RNA polymerase promoter;
- (ii) a third DNA sequence encoding a P protein of the vesiculovirus; and
- 15 (iii) a third transcription termination signal for the RNA polymerase;

(d) a fourth DNA plasmid vector comprising the following operatively linked components:

- 20 (i) the bacteriophage RNA polymerase promoter;
- (ii) a fourth DNA sequence encoding an L protein of the vesiculovirus; and
- (iii) a fourth transcription termination signal for the RNA polymerase; and

25 (e) a recombinant vaccinia virus comprising a sequence encoding the bacteriophage RNA polymerase; whereby in said cell the first DNA sequence is transcribed to produce said RNA molecule, the N, P, and L proteins and the bacteriophage RNA polymerase are expressed, and a recombinant
30 replicable vesiculovirus is produced that has a genome that is the complement of said antigenomic RNA comprising said foreign RNA sequence.

34. A vaccine formulation comprising an effective
35 immunizing amount of the vesiculovirus of claim 3; and a pharmaceutically acceptable carrier.

35. A vaccine formulation comprising an effective immunizing amount of the recombinant vesiculovirus of claim 4; and a pharmaceutically acceptable carrier.

5 36. A vaccine formulation comprising an effective immunizing amount of the recombinant vesiculovirus of claim 10; and a pharmaceutically acceptable carrier.

37. A vaccine formulation comprising an effective
10 immunizing amount of a first recombinant vesiculovirus of claim 3; an effective immunizing amount of a second recombinant vesiculovirus of claim 3; and a pharmaceutically acceptable carrier; in which said peptide or protein expressed by the first and second recombinant vesiculoviruses
15 are different.

38. The vaccine formulation of claim 37 in which the peptide or protein expressed by the first recombinant vesiculovirus displays the antigenicity or immunogenicity of
20 an antigen of a first pathogenic microorganism, and the peptide or protein expressed by the second recombinant vesiculovirus displays the antigenicity or immunogenicity of an antigen of a second, different pathogenic microorganism.

25 39. A method of treating or preventing a disease or disorder in a subject comprising administering to the subject an effective immunizing amount of the recombinant vesiculovirus of claim 3.

30 40. A method of treating or preventing a disease or disorder in a subject caused by infection by a pathogenic microorganism comprising administering to the subject an effective immunizing amount of the recombinant vesiculovirus of claim 4.

35 41. A method of treating or preventing a subject having a tumor comprising administering to the subject an

effective immunizing amount of the recombinant vesiculovirus of claim 10.

42. The method according to claim 39 in which the
5 subject is a human.

43. The method according to claim 39 in which the
subject is a non-human animal.

10 44. A kit comprising in one or more containers (a)
a first recombinant nucleic acid that can be transcribed in a
host cell to produce an RNA molecule comprising a
vesiculovirus antigenomic (+) RNA, in which a region of the
RNA nonessential for replication of the vesiculovirus has
15 been inserted into or replaced by a foreign RNA sequence; (b)
a second recombinant nucleic acid encoding and capable of
expressing in the host cell a vesiculovirus N protein; (c) a
third recombinant nucleic acid encoding and capable of
expressing in the host cell a vesiculovirus-L protein; and
20 (d) a fourth recombinant nucleic acid encoding and capable of
expressing in the host cell a vesiculovirus P protein.

45. A kit comprising in one or more containers (a)
a first recombinant nucleic acid that can be transcribed in a
25 host cell to produce an RNA molecule comprising a
vesiculovirus antigenomic (+) RNA; (b) a second recombinant
nucleic acid encoding and capable of expressing in the host
cell a vesiculovirus N protein; (c) a third recombinant
nucleic acid encoding and capable of expressing in the host
30 cell a vesiculovirus L protein; and (d) a fourth recombinant
nucleic acid encoding and capable of expressing in the host
cell a vesiculovirus P protein.

46. A kit comprising in one or more containers (a)
35 a recombinant nucleic acid that can be transcribed to produce
an RNA molecule comprising a vesiculovirus antigenomic (+)

RNA; and (b) a host cell that recombinantly expresses vesiculovirus N, P, and L proteins.

47. The kit of claim 45 in which said first
5 recombinant nucleic acid further comprises a polylinker in a region that is transcribed to produce said RNA molecule, said region being nonessential for replication of the vesiculovirus.

10 48. The kit according to claim 45 in which the second recombinant nucleic acid is a DNA plasmid vector comprising the following operatively linked components:

- (a) a promoter which controls the expression of the N protein;
- 15 (b) a translation initiation signal;
- (c) a DNA sequence encoding the N protein; and

(d) a transcription termination signal; and
in which the third recombinant nucleic acid is a DNA plasmid
20 vector comprising the following operatively linked components:

- (a) a promoter which controls the expression of the P protein;
- (b) a translation initiation signal;
- 25 (c) a DNA sequence encoding the P protein; and

(d) a transcription termination signal
and in which the fourth recombinant nucleic acid is a DNA
plasmid vector comprising the following operatively linked
30 components:

- (a) a promoter which controls the expression of the L protein;
- (b) a translation initiation signal;
- (c) a DNA sequence encoding the L protein; and
- 35 (d) a transcription termination signal; and

in which the first recombinant nucleic acid is a DNA plasmid vector comprising the following operatively linked components:

- (a) a promoter;
- 5 (b) a DNA sequence that can be transcribed under the control of the promoter in the cell to produce said RNA molecule, said RNA molecule further comprising a ribozyme sequence immediately downstream of said antigenomic (+) RNA, that cleaves at the 3' terminus of the antigenomic (+) RNA, said DNA comprising a polylinker in a region that is transcribed to produce said RNA molecule, said region being
10 nonessential for replication of the vesiculovirus; and
- 15 (c) a transcription termination signal.

49. The kit of claim 48 in which the promoter is
20 an RNA polymerase promoter, and in which the cell also contains a cytoplasmic source of said RNA polymerase.

50. A kit comprising

- (a) in a first container a first DNA plasmid
25 vector comprising the following operatively linked components:
 - (i) a bacteriophage RNA polymerase promoter;
 - (ii) a first DNA sequence that can be transcribed in a cell to produce an RNA molecule comprising (A) a vesiculovirus antigenomic (+) RNA in which a region of the RNA nonessential for replication of the vesiculovirus has been inserted into or replaced by a foreign RNA sequence,
30 and (B) a ribozyme sequence immediately downstream of said antigenomic (+) RNA,

- that cleaves at the 3' terminus of the antigenomic RNA; and
- (iii) a transcription termination signal for the RNA polymerase;
- 5 (b) in a second container a second DNA plasmid vector comprising the following operatively linked components:
- (i) the bacteriophage RNA polymerase promoter;
- 10 (ii) a second DNA sequence encoding an N protein of the vesiculovirus; and
- (iii) a second transcription termination signal for the RNA polymerase;
- (c) in a third container a third DNA plasmid
- 15 vector comprising the following operatively linked components:
- (i) the bacteriophage RNA polymerase promoter;
- (ii) a third DNA sequence encoding a P protein
- 20 of the vesiculovirus; and
- (iii) a third transcription termination signal for the RNA polymerase;
- (d) in a fourth container a fourth DNA plasmid vector comprising the following operatively linked
- 25 components:
- (i) the bacteriophage RNA polymerase promoter;
- (ii) a fourth DNA sequence encoding an L protein of the vesiculovirus; and
- 30 (iii) a fourth transcription termination signal for the RNA polymerase; and
- (e) in a fifth container a recombinant vaccinia virus comprising a sequence encoding the bacteriophage RNA polymerase.
- 35
51. A kit comprising in a container an effective immunizing amount of the vesiculovirus of claim 3.

52. The vesiculovirus of claim 1 which is a vesicular stomatitis virus.

53. The vesiculovirus of claim 4 in which the peptide or protein displays the antigenicity or immunogenicity of an envelope glycoprotein of a virus other than a vesiculovirus.

54. The vesiculovirus of claim 53 in which the envelope glycoprotein is an envelope glycoprotein of a Human Immunodeficiency Virus.

55. The vesiculovirus of claim 53 in which the peptide or protein is incorporated into the vesiculovirus envelope.

56. The vesiculovirus of claim 53 in which the peptide or protein is expressed as a fusion protein comprising the cytoplasmic domain of a vesiculovirus G protein.

57. The vesiculovirus of claim 56 in which the native G protein of the vesiculovirus is not expressed.

58. The vesiculovirus of claim 56 in which the native G protein of the vesiculovirus is also expressed.

59. The vesiculovirus of claim 3 in which a second RNA sequence complementary to said foreign RNA sequence encodes a second peptide or protein that is expressed in the suitable host, in which the first peptide or protein and the second peptide or protein display different antigenicity or immunogenicity.

60. An inactivated recombinant vesiculovirus that is the product of a method comprising inactivating a recombinant replicable vesiculovirus, the genome of which

comprises a foreign RNA sequence, in which an RNA sequence complementary to said foreign RNA sequence encodes a peptide or protein that is expressed in a suitable host infected by the recombinant replicable vesiculovirus, and in which the
5 peptide or protein is antigenic or immunogenic.

61. The vesiculovirus of claim 60 in which the peptide or protein displays the antigenicity or immunogenicity of an antigen of a pathogenic microorganism.

10

62. The vesiculovirus of claim 60 in which the peptide or protein displays the antigenicity or immunogenicity of a tumor specific or tumor associated antigen.

15

63. The vesiculovirus of claim 60 in which a second RNA sequence complementary to said foreign RNA sequence encodes a second peptide or protein that is expressed in the suitable host, in which the first peptide or
20 protein and the second peptide or protein display different antigenicity or immunogenicity.

64. The vesiculovirus of claim 60 in which the peptide or protein displays the antigenicity or
25 immunogenicity of an envelope glycoprotein of a virus other than a vesiculovirus.

65. The vesiculovirus of claim 64 in which the envelope glycoprotein is an envelope glycoprotein of a Human
30 Immunodeficiency Virus.

66. The vesiculovirus of claim 64 in which the peptide or protein is incorporated into the vesiculovirus envelope.

35

67. The vesiculovirus of claim 64 in which the peptide or protein is expressed as a fusion protein

comprising the cytoplasmic domain of a vesiculovirus G protein.

68. A vaccine formulation comprising an effective
5 immunizing amount of the vesiculovirus of claim 60; and a
pharmaceutically acceptable carrier.

69. A vaccine formulation comprising an effective
immunizing amount of the vesiculovirus of claim 64; and a
10 pharmaceutically acceptable carrier.

70. A vaccine formulation comprising an effective
immunizing amount of the vesiculovirus of claim 66; and a
pharmaceutically acceptable carrier.

15

71. A method of treating or preventing a disease
or disorder in a subject comprising administering to the
subject an effective immunizing amount of the inactivated
recombinant vesiculovirus of claim 60.

20

72. A kit comprising in a container an effective
immunizing amount of the inactivated recombinant
vesiculovirus of claim 60.

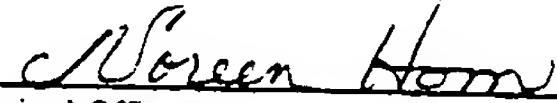

25

73. A method for producing a peptide or protein
comprising culturing a cell containing the recombinant
replicable vesiculovirus of claim 2 in said suitable host;
and recovering the expressed peptide or protein.

30

74. A method for producing an inactivated virus
vaccine comprising inactivating a recombinant replicable
vesiculovirus, the genome of which comprises a foreign RNA
sequence, in which an RNA sequence complementary to said
foreign RNA sequence encodes a peptide or protein that is
35 expressed in a suitable host infected by the recombinant
replicable vesiculovirus, and in which the peptide or protein
is antigenic or immunogenic.

International Application No: PCT/

MICROORGANISMS	
Optional Sheet in connection with the microorganism referred to on page 71, lines 15-35 of the description	
A. IDENTIFICATION OF DEPOSIT	
Further deposits are identified on an additional sheet	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, MD 20852 US	
Date of deposit: May 2, 1995 Accession Number: 97134	
B. ADDITIONAL INDICATIONS (leave blank if not applicable). This information is continued on a separate attached sheet	
C. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not all designated States)	
D. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (Specify the general nature of the indications e.g., "Accession Number of Deposit")	
E. <input checked="" type="checkbox"/> This sheet was received with the International application when filed (to be checked by the receiving Office)	
<div style="text-align: right;"> (Authorized Officer)</div>	
<input type="checkbox"/> The date of receipt (from the applicant) by the International Bureau	
was	
<div style="text-align: right;"> (Authorized Officer)</div>	

Form PCT/RO/134 (January 1981)

1/50

90
CACCTAAATGTAAGCGTTAATAATTTGTTAAATTCGGCTTAAATTTTGTAAATCAGCTCATTTTTTAAACCAATAGCCCGAAATCGG
GTGGATTTAACATTCGCAATTATAAAACAATTTAAGCCCAATTTAAAAACAATTTAGTCGAGTAAAAAATTCGTTATCCGGCTTAGCC

180
CAAAATCCCTTATAAATCAAAAGAAATAGACCGAGATAGCGTTGAGTGTGTTCCAGTTTGGAACAAGATCCACTATTAAAGAACGTGGA
GTTTTAGGGAATATTAGTTTCTTATCTGGCTCTATCCCAACTCACAACAAGTCAAAACCTTGTTCICAGGTGATAAATTTCTTGCACCT

BsaI 1
CTCCAACGTCAAAGCGCGAAAAACCGTCTATCAGGGCGATGCCCCACTACGTGAACCATCACCTTAATCAAGTTTTTGGGTGAGGTG
GAGGTGTCAGTTTCCCGCTTTTGGCAGATAGTCCCGCTACCGGTGATGCACCTTGGTAGTGGGATTAGTTCAAAAAACCCAGCTCCAC

270
CCGTAAAGCACIAAATCGGAACCTTAAGGGAGCCCCCGATTAGAGCTTGACGGGAAGCCGGCAACGTGGCGAGAAAGGAGGAA
GGCATTTCTGTATTAGCCTTGGGATTTCCTTCGGGGGCTAAATCTCGAACATGCCCCCTTCGGCCGCTTGCACCGCTCTTCCCTTCCCTT

360
GAAAGCGAAAGGAGCGGGCTAGGGCGCTGGCAAGTGTAGCGGTACGGCTGCGCGTAACCAACACACCCGCGCGCTTAATGCGCCGCT
CTTTCCGCTTTCCTCGCCCGGATCCCGGACCGTTACATCGCCAGTGGACGGCGCATTTGGTGGTGGCGGGCGGAATTACGGCGCGGA

450
ACAGGCGCGTCCCATTCGCCATTACGGCTGCGCAACTGTGGGAAGGGCGATCGGTGCGGGCTCTTCGCTATTACGCCAGCTGCGCGAA
TGTCGGCGCAGGGTAAGCGGTAAATCGGACCGGTGACAAACCTTCCCGCTAGCCACCGCGGAGAGCGGATAATGCGGTGACCGCTT

540

FIG.1A

SUBSTITUTE SHEET (RULE 26)

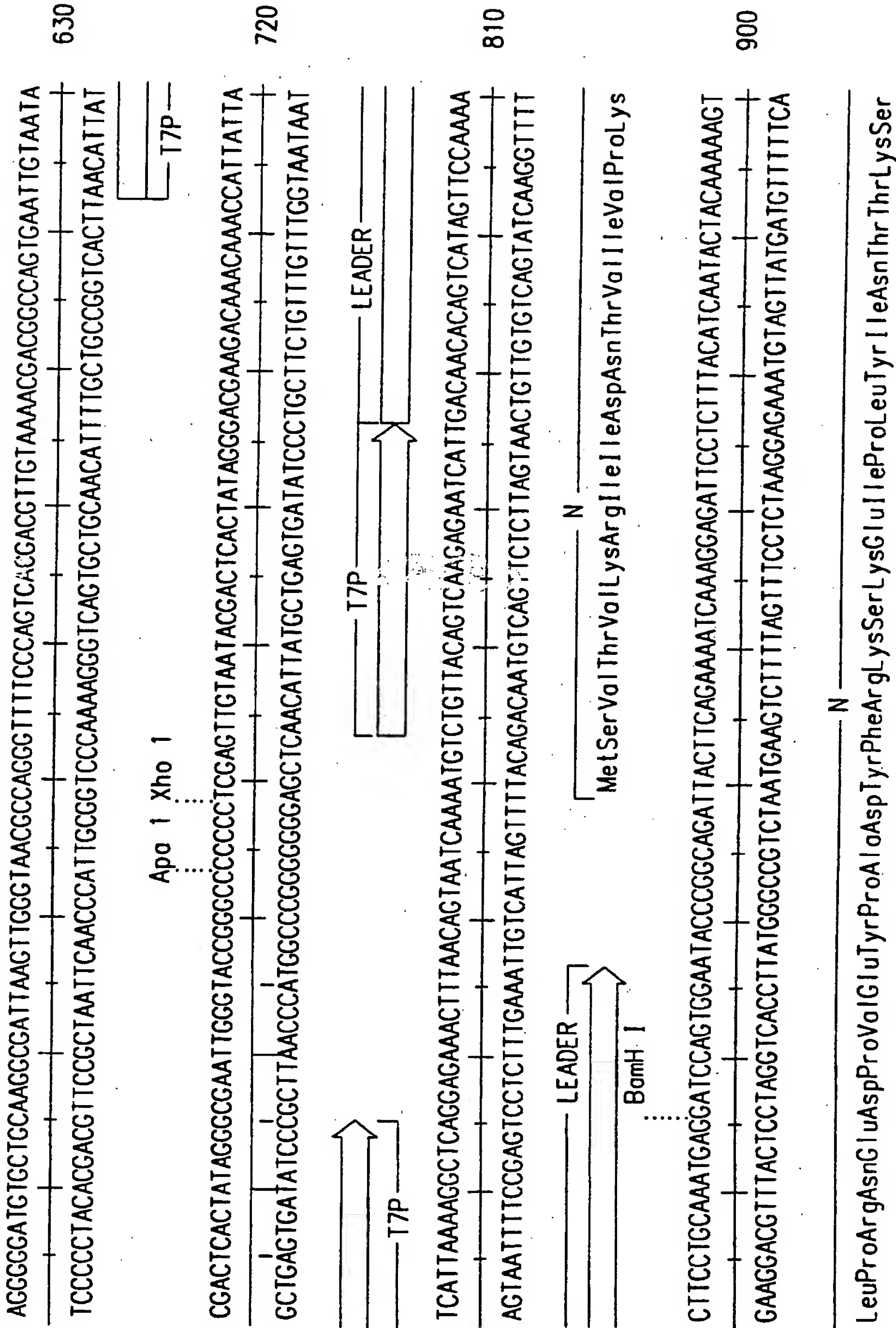


FIG.1B

SUBSTITUTE SHEET (RULE 26)

TTGTCAGATCTAAGAGGATAIGTCTACCAAGCCTCAAAATCCGGAATGTATCA/TCTATACATGTCACACAGCTACTTGTATGGACCATTA
AACAGTCTAGATTCTCCTATACAGATGGTTCGGAGTTTACGCCCCTTACATAGTTA³TAIGTACAGTTGTCGATGAACATACCTCGTAAT

990

LeuSerAspLeuArgGlyTyrValTyrGlnGlyLeuLysSerGlyAsnValSerIleIleHisValAsnSerTyrLeuTyrGlyArgLeu

AAGACATCCGGGTAAGTTGGATAAAGATTGGTCAAGTTTCGGAATAACATCGGGAACGAGGGATACAAATCGGAATATTGACCTT
TTCCTGTAGGCCCCATTCAACCTATTICTAACCCAGTTCAAAGCCTTATTGTAGCCCTTTCGTCCCTTAGCTTAGCCTTATAAACATGGAA

1080

LysAspIleArgGlyLysLeuAspLysAspTrpSerSerPheGlyIleAsnIleGlyLysAlaGlyAspThrIleGlyIlePheAspLeu

GTATCCTTGAAGCCCCTGGACGGGTACTTCCAGATGGAGTATCGGATGCTTCCAGAACCAGCCGAGATGACAAATGGTTCCTTTGTAT
CATAGGAAGTTTCGGGACCTGCCCGCATGAAGGTCTACCTCATAGCCTACGAAGGTCTTCGTCCGCTCTACGTTTACCAACGGAAACATA

1170

ValSerLeuLysAlaLeuAspGlyValLeuProAspGlyValSerAspAlaSerArgThrSerAlaAspLysTrpLeuProLeuTyr

CTACTTCGCTTATACAGAGTGGCCAGACACAAATGCCCTGAATACAGAAAAGCTCATGATCGGCIGACAAATCAATGCAAAATGATC
GATGAACCGAAATATGTCACCCGCTGTGTTACGGACTTATGTCCTTTTTCGAGTACCTACCCGACTGTTTAGTTACGTTTACTAG

1260

LeuLeuGlyLeuTyrArgValGlyArgThrGlnMetProGluTyrArgLysLysLeuMetAspGlyLeuThrAsnGlnCysLysMetIle

FIG.1C

1350
 AATGAACAGTTTGAACCTCTTGTGCCAGAAGGTCGTGACATTTTIGATGTGTCGGGAAATGACAGTAATTACACAAAAATTGTCGTGCA
 TTAATGTCGCAAACTTGGAGAACACGGTCTTCCAGCACTGTAAAACTACACACCCCTTACTGTCATTAAATGTTTAAACACCGACGT
 N
 AsnGluGlnPheGluProLeuValProGluGlyArgAspIlePheAspValTrpGlyAsnAspSerAsnTyrThrLysIleValAlaIle
 GTGGACAATGTTTCCACATGTTCAAAAAACATGAATGTCCTCGTTTCAGATACGGAACATATGTTCCAGATTCAAAAGATTGTCGTGCA
 1440
 CACCTGTACAAGAAGGTGTACAAGTTTGTGTTTACTTACACGGAGCAAGTCTATGCCCTTCATACAAAGGTCTAAGTTTCTAACACCGACGT
 N
 ValAspMetPhePheHisMetPheLysLysHisGluCysAlaSerPheArgTyrGlyThrIleValSerArgPheLysAspCysAlaIle
 TTGGCAACATTTGGACACCTCTGCAAAATAACCGGAATGTTACAGAGAATGTAAGGACCTGGAATCTGAACCGAGAAGTTGCAGATGAA
 1530
 AACCGTTGTAAACCTGTGGAGACGTTTATGGCCTTACAGATGTTCTTACATTCCTGGACCTAGAACCTGGCTCTTCAACGTTCTACTT
 N
 LeuAlaThrPheGlyHisLeuCysLysIleThrGlyMetSerThrGluAspValThrThrTrpIleLeuAsnArgGluValAlaAspGlu
 ATGGTCCAAATGATGCTTCCAGGCCAAGAAATGACAGGCCCGATTATATGATGCTTATGATGCTTATGATGCTTATGATGCTTATGATGCT
 1620
 TACCAGGTTTACTACGAAGGTCCGGTCTTTAACGTTCCGGCTAAGTATGTACCGAATAAATAGCTGAAACCTAACAGAAAGATTACAGA
 N
 MetValGlnMetMetLeuProGlyGlnGluIleAspLysAlaAspSerTyrMetProTyrLeuIleAspPheGlyLeuSerSerLysSer

FIG.1D

CCATATTCTCCGTCACAAACCCIGCCCTCCACTTCIGGGGCAATTCACAGCTCTCTGCTCAGATCCACGAGCAAGGAATGCCCCGA
GGTATAAGAAGCCAGTTTIGGGACGGAAGGTGAAGACCCCGTTAACTGTCCAGAGA GACGAGTCTAGGTGCTCGTTCCTTACGGGCT 1710

ProTyrSerSerValLysAsnProAlaPheHisPheTrpGlyGlnLeuThrAlaLeuLeuArgSerThrArgAlaArgAsnAlaArg

Bst1107 1

Bam H 1

CAGCCTGATGACATTGAGTATACATCTCTTACTACAGCAGGTTCGTGTACGCTTATGCAGTAGGATCCCTCTGCCGACTTGGCACAACAG
GTCCGACTACGTAACTCATACTAGAGAAATGATGCTGCCAAACAACATGCCGAATACGTCTATCCCTAGGAGACGGCTGAACCGTGTGTC 1800

GlnProAspAspIleGluTyrThrSerLeuThrThrAlaGlyLeuLeuTyrAlaTyrAlaValGlySerSerAlaAspLeuAlaGlnGln

TTTGTGTGGAGATAACAAATACACICCAGATGATAGTACCGGAGGATTGACGACTAATGCCACCGCCCAAGCCAGAGATGTGTCGAA
AAACACAAACCCTCTATGTGTTAIGTGAGGCTCTACTATCATGCCCCTCCTAACTGCTGATTACGTGGCGGTGTCCGCTCTACACCCAGCTT 1890

PheCysValGlyAspAsnLysTyrThrProAspAspSerThrGlyGlyLeuThrThrAsnAlaProProGlnGlyArgAspValValGlu

FIG.1E

1980
TGGCTCGGATGGTTGAAGATCAAAACAGAAACCGACCTCTGATATGATGCAGTATCGGAAAAGAGCCAGTCAIGTCACIGCAAGGCCCTA
ACCGAGCCTACCAAACCTCTAGTTTGTCTTTTGGCTGAGGACTATACTACGTCAACCGCTTTTCTCGTCAGTACAGTGACGTTCCGGAT
N
TrpLeuGlyTrpPheGluAspGlnAsnArgLysProThrProAspMetMetGlnTyrAlaLysArgAlaValMetSerLeuGlnGlyLeu
2070
AGAGAGAAGACAATTGGCAAGTAIGCTAAGTCAGAAATTGACAAAATGACCCCTATAATTCTCAGATCACCTATTATATATTATGCTACATA
TCCTCTTCTGTAAACCGTTCATACGATTACGATTAACACGTTTACTGGGATATTAAGAGCTAGTGGATAATATAATACGATGAT
N
ArgGluLysThrIleGlyLysTyrAlaLysSerGluPheAspLys
2160
TGAAAAAACTAACAGATAICATGGATAATCICACAAAAGTTCGTGAGTATCICAAGTCTATTCGTCTGGATCAGGCCGTAGGAGAG
ACTTTTTTGTGATGCTATAGTACCTATTAGAGTGTTCAGGACTCATAGAGTTCAGGATAAGAGCAGACCTAGTCCGCCCAICCTCTC
P
MetAspAsnLeuThrLysValArgGluTyrLeuLysSerTyrSerArgLeuAspGlnAlaValGlyGlu
2250
ATAGATGAGATCGAAGCACAACGAGCTGAAAAGTCCAAATTATGAGTTGTTCCAAGAGGATGGAGTGGAAAGCATACTAAGCCCCTCTAT
TATCTACTAGCTTCGTGCTCGACTTTTCAGGTTAATACICAACAAGGTTCTCCTACCTCACCTTCCTGTAIGATTTCGGGAGAATA
P
IleAspGluIleGluAlaGlnArgAlaGluLysSerAsnTyrGluLeuPheGlnGluAspGlyValGluGluHisThrLysProSerTyr

FIG.1F

TTTCAGGCAGCAGATGATCTGACACAGAACTGAACCAGAAATGAAGACAATCAAGTTIGTATGCACCAGATCCAGAAGCTGAGCAA
AAAGTCCGTCGTCCTACTAAGACTGIGTCTTAGACTTGGTCTTTAAGTCTTCTAGCTTCCAAACATACGTGGTCTAGGCTCTCGACTCGTT
PheGlnAlaAlaAspAspSerAspThrGluSerGluProGluIleGluAspAsnGlyLeuTyrAlaProAspProGluAlaGluGln
GTTGAAGCCTTTATACAGGGCCTTTAGATGACTATGCAGATGAGGAAGTGAIGTGTATTACTTCGGACTGGAAACAGCCCTGAGCTT
CAACTCCGAAATATGTCGCCGGAATCTACTGATACGTCTACTCTTCACTTACCAACATAAATGAAGCCTGACCTTGTCCGACTCGAA
ValGluGlyPheIleGlnGlyProLeuAspTyrAlaAspGluGluValPheThrSerAspTrpLysGlnProGluLeu
GAATCTGACGAGCATGGAAAGACCTTACGGTTGACATGCCAGAGGGTTAAGTGGAGAGCAGAAATCCCAGTGGCTTTCGACGATTAA
CTTAGACTGCTCGTACCTTCTCGAATGCCAACIGTAGCGGTCTCCCAATTCACCTCTCGTCTTAGGGTCACCGAAAGCTGCTAATTT
GluSerAspGluHisGlyLysThrLeuArgLeuThrSerProGluGlyLeuSerGlyGluGlnLysSerGlnTrpLeuSerThrIleLys
GCAGTCGTCCAAGTCCCAAATACTGGAACTCGCAGAGTGCACATTTGAAGCATCGGGAGAGGGGTCAATTATGAAGAGCGCCAGATA
CGTCAGCAGCTTTCACGGTTATGACCTTAGACCGTCTACCGTGAACCTCGTACCCCTCTTCCCAGTAATACTTCCCGGCTCTAT
AlaValValGlnSerAlaLysTyrTrpAsnLeuAlaGluCysThrPheGluAlaSerGlyGluGlyValIleMetLysGluArgGlnIle

FIG.1G

ThrProAspValTyrLysValThrProValMetAsnThrHisProSerGlnSerGluAlaValSerAspValTrpSerLeuSerLysThr

Xba 1

...

TCCA TGAC TTCCA ACCCAAGAAAGCAAGCTTCAGCCTCTCACCATACTCTTGGATGAATGTTCTCATCTAGAGGAGAGTTCAATCTCT

AGGTACTGAAGGTGGTTCCTTCGTTCAGAAAGTCGGAGAGTGGTATAGGAACCTACTTAACAAGAGTAGAICTCCCTCTCAAGTAGAGA

2790

SerMetThrPheGlnProLysAlaSerLeuGlnProLeuThrIleSerLeuAspGluLeuPheSerArgGlyGluPheIleSer
 _____P_____

GTCCGAGGTGACGGACGAAIGTCICATAAAGAGGCCATCCIGCTCGCCTGAGATACAAAAGTTGTACAATCAGCGGAGAGTCAAATAT
 CAGCCTCCACTGCCCTGCTTACAGAGTATTICCCGGTAGGACGAGCCGGACTCTATGTTTTCAACATGTTAGTCCGCTCTCAGTTTATA
 2880

ValGlyGlyAspGlyArgMetSerHisLysGluAlaIleLeuLeuGlyLeuArgTyrLysLysLeuTyrAsnGlnAlaArgValLysTyr

FIG. 1H

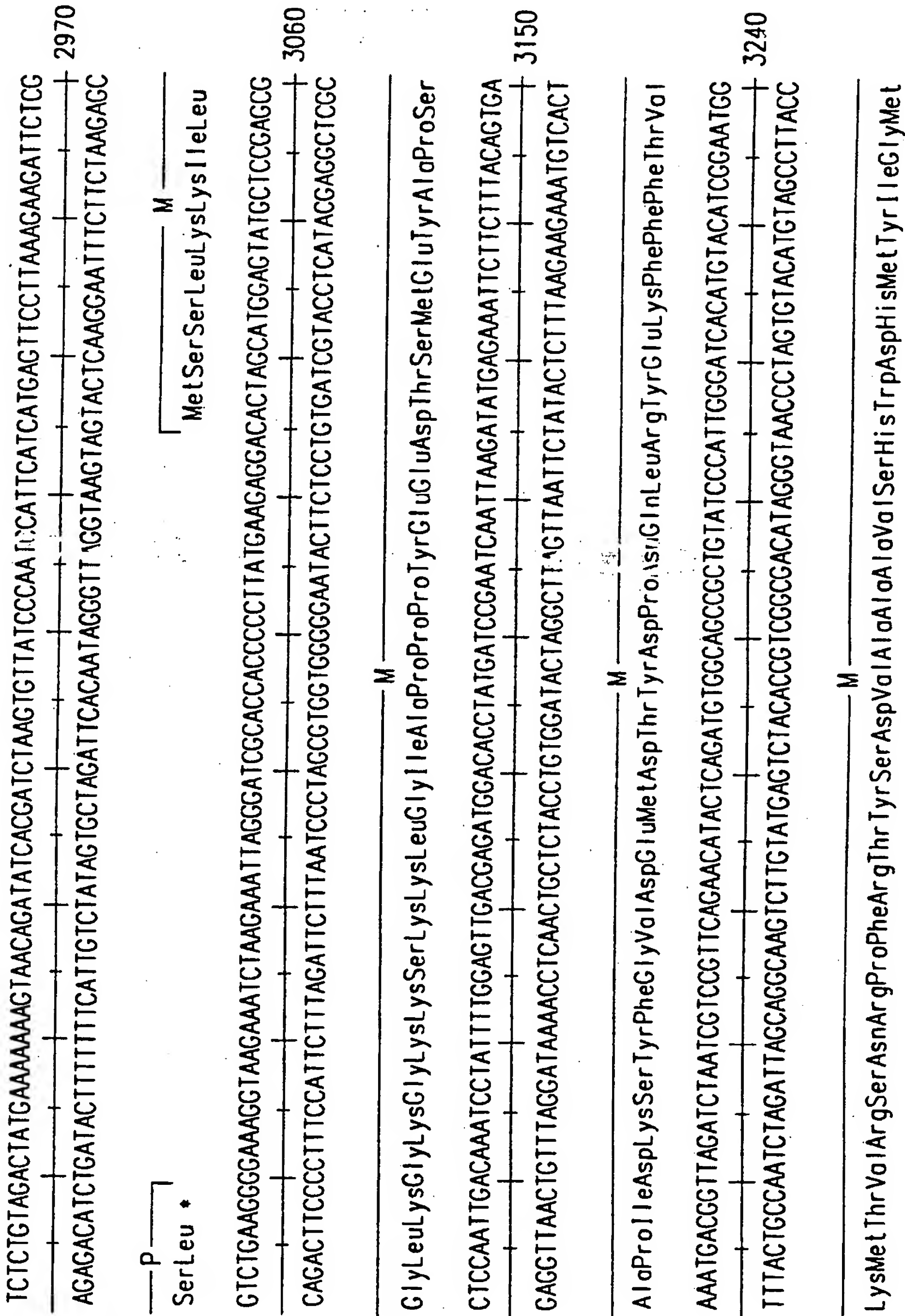


FIG. 11

CAGGGAACGTCCTTCTACAAAATCTGGCTTTTIGGGTTCCTAATCTAAAGGCCACTCCAGCGGTATIGGCAGATCAAGGTCAAC
GTCCCTTTGCAGCGAAGATGTTTAGAACCGGAAACCAAGAGATTAGATTTCCGGTGAGGTGCCCATAACCGTCTAGTTCAGTTG 3330

AlaGlyLysArgProPheTyrLysIleLeuAlaPheLeuGlySerSerAsnLeuLysAlaThrProAlaValLeuAlaAspGlnGlyGln M

CAGAGTATCACACTCACATCCGAAGCGAGGGCTTATTGCCACATAGGATGGGAAGACCCCTCCCATGCTCAATGTACCAGAGCACTTCA
GTCTCATAGTGTGAGTGACCGCTCCGTCGCCGAATAAACGGTGATCCTACCCCTTCTGGGAGGGTACGAGTTACATGGTCTCGTGAAGT 3420

ProGluTyrHisThrHisCysGluGlyArgAlaTyrLeuProHisArgMetGlyLysThrProProMetLeuAsnValProGluHisPhe M

Sac 1

GAAGACCATTCATAATAGGTCCTTACAAGGGAACGATTGACCTCACAAATGACCATCTACGATGATGAGTCACTGGAAGCAGCTCCTATGA
CTTCTGGTAAGTTATATCCAGAAATGTTCCTTGCTAACTCGAGTGTACIGGTAGATGCTACTACTCAGTGACCTTCGTCGAGGATACT 3510

ArgArgProPheAsnIleGlyLeuTyrLysGlyThrIleGluLeuThrMetThrIleTyrAspAspGluSerLeuGluAlaAlaProMet M

FIG.1J

TCIGGATCAATTCCTCAATTTCTGATTTTCAGAGAGAGGCCCTTAAT,TTGGCCCTGATTCGAGAGAGGCCATCIGGAG
AGACCCTAGTAAAGTTAAGAAGTTTAAAGACTAAAGTCCTCTCTCCGGAATTA,AAACCGGACTAACAGGCCTCTTTTCCGTAGACCTC 3600

IleTrpAspHisPheAsnSerSerLysPheSerAspPheArgGluLysAlaLeuMetPheGlyLeuIleValGluLysLysAlaSerGly
CGTGGTCCCTGGATTCTATCAGCCCACTTCAAATGAGCTAGCTAAGTTCTAGCTTCTGAACAATCCCGGTTTACTCAGTCCTCTCTAAT 3690
GCACCCAGGACCTAAGATAGTCGGTGAAGTTTACTCCATCAGATGAAGATCCAAGACTTGTAGGGGCCAAATGAGTCAGAGAGGATTA

AlaTrpValLeuAspSerIleSerHisPheLys *

Mlu 1
TCCAGCCCTCAGAACAACTAATACCTGCTCTTTTCTATCCCTATGAAAAAACTAACAGAGATCGATCIGTTACCGGTCACCTATGAAGT
AGTCCGAGAGCTTGTGATTATAGGACAGAAAAGATAGGATACTTTTTTTCATGCTCTCTAGCTAGACAAATGCCCAGTGATACTTCA 3780

G-
MetLys

FIG.1K

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GCCTTTGTACTAGCCTTTTATTCATGGGGTGAATTGCAAGTTCACCATAGTTTTCCACACAACCAAAAGGAAACTGGAAAAATG
CGGAAACATGATCGGAAAAATAAGTAACCCCACTTAACGTTCAGTGGTATCAAAAAGGTGCTGCTTTTCCCTTTGACCTTTTAC 3870

CysLeuLeuTyrLeuAlaPheLuePheIleGlyValAsnCysLysPheThrIleValPheProHisAsnGlnLysGlyAsnTrpLysAsn

Swa 1

TTCCCTTCTAATTACCATTAATGCCCCGTCAGCTCAGATTTAAATTGGCATAATGACTTAATAGGCACAGCCATACAAGTCAAAATGCCCA
AAGGAAGATTAAATCGTAATAACGGGCAGTTCGAGTCTAAATTAAACCGTATTACGAATTATCCGTGTCGGTATGTTACAGTTTACCGGT 3960

ValProSerAsnTyrHisTyrCysProSerSerSerAspLeuAsnTrpHisAsnAspLeuIleGlyThrAlaIleGlnValLysMetPro

AGAGTCACAAGGCTATTCAGCAGACCGTTGGAATGTCATGCTTCCAAATGGGTACTACTTGCTGATTTCGGCTGGTATGGACCGAAGT
TCTCAGTGTCCGATAAGTTCGTCGCCAACCACACAGTACGAAGTTTACCCAGTGAACACTAAAGCGGACCATACCTGGCTTCA 4050

LysSerHisLysAlaIleGlnAlaAspGlyTrpMetCysHisAlaSerLysTrpValThrThrCysAspPheArgTrpTyrGlyProLys

FIG.1L

ATATAACACAGTCCGATCCCTTCACICCATCTGTAGAACAATGCAAGGAAGCAATTGAACAAACGAAACGAACCTGGCTGAATC
 TATATTGTCAGTAGGCTAGGAAGTAGGATGACATCTGTGTACGTTCCCTTCTTAACTGTGTGCTTGTCTTGAACCGACTTAG
 4140
 G
 Tyr Ile Thr Glu Ser Ile Arg Ser Phe Thr Pro Ser Val Glu Glu In Cys Lys Glu Ser Ile Glu Glu In Thr Lys Glu Gly Thr Trp Leu Asn
 CAGGCTTCCCTCCCTCAAAGTGTGGATATGCAACTGTACCGGATGCCGAAGCAGTATATGTCCAGGTGACTCCCTCACCATTGCTGGTTG
 GTCCGAAGGGAGGAGTTTCAACACCTATACGTTGACACTGCCCTACGGCTTCGTCACCTAACAGGTCCACTGAGGAGTGGTACACGACCAAC
 4230
 G
 Pro Gly Phe Pro Pro Glu Ser Cys Gly Tyr Ala Thr Val Thr Asp Ala Glu Ala Val Ile Val Glu In Val Thr Pro His His Val Leu Val
 ATGAATACACAGGAGAAATGGGTGTGATTCACAGTTCATCAACGGAATAATGAGCAATATACATATGCCCCACTGTCCATAACTCTACAACCT
 TACTTATGTGTCCTCTTACCCCACTAAGTGTCAAGTAGTGGCTTTACGTCGTTAATGATACGGGGTGACAGGTATTCAGATGTTGGA
 4320
 G
 Asp Glu Tyr Thr Gly Glu Trp Val Asp Ser Glu Phe Ile Asn Gly Lys Cys Ser Asn Tyr Ile Cys Pro Thr Val His Asn Ser Thr Thr
 GGCATTCTGACTATAAGGTCAAAGGCTATGTGATTCCTAACCTCATTTCCATGCCACATCACCTTCTTCTCAGAGCAGGAGCTATCAT
 CCGTAAGACTGATATCCAGTTTCCCGATACACTAAGATTGGAGTAAAGTACCTGTAGTGGGAAGAAGAGTCTCCCTGCTCCGATAGTA
 4410
 G
 Trp His Ser Asp Tyr Lys Val Lys Gly Leu Cys Asp Ser Asn Leu Ile Ser Met Asp Ile Thr Phe Phe Ser Glu Asp Gly Glu Leu Ser

FIG. 1M

CCCTGGGAAAGGAGCGGCACAGGGTTCAGAGTAACACTACTTTCCTTAIGAAACTGGAGCAAGCCTGC AAAATGCAATACTGCAAGCAATT
GGGACCCCTTTCCTCCCGTGTCCTCAAGTCTTCATTTGATGAACGGAATACTTTGACCTCCGTTCGGGACGTTTACGTTAIGACGTTGCTAA 4500

-----G-----
SerLeuGlyLysGluGlyThrGlyPheArgSerAsnTyrPheAlaTyrGluThrGlyGlyLysAlaCysLysMetGlnTyrCysLysHis

GGGGAGTCAGACTCCCATCAGGTGTCIGGTTCGAGATGGCTGATAAGGATCTCTTTGCTCCAGCCAGATTCCCTGAAATGCCCAAGAGGT
CCCCICAGTCTGAGGGTAGTCCACAGACCAAGCTCTACCGACTATTCCTAGAGAAACGACGTCGGTCTAAGGGACTTACGGGTCCTCCCA 4590

-----G-----
TrpGlyValArgLeuProSerGlyValTrpPheGluMetAlaAspLysAspLeuPheAlaAlaArgPheProGluCysProGluGly

CAAGTATCTCTGCTCCATCTCAGACCTCAGTGGATGTAAGTCTAATTCAGGACGTTGAGAGGAICTTGGATTATTCCTTCCTGCCAAGAAA
GTTCAAGAGACGAGGTAGAGTCTGGAGTCACCTACATTACAGTTAAGTCTGCAACTCTCCTAGAACCTAATAAGGGAGACGGTCTCTTT 4680

-----G-----
SerSerIleSerAlaProSerGlnThrSerValAspValSerLeuIleGlnAspValGluArgIleLeuAspTyrSerLeuCysGlnGlu

CCTGGAGCAAATCAGACGGGCTCTCCAATCTCTCCAGTGGATCTCAGCTATCTGCTCCTAAAAACCCAGGAACCGGTCTCTTTCA
GGACCICGTTTTAGTCTCGCCCCAGAGGTTAGAGAGGTCACCTAGAGTCGATAGAACGAGGATTTTGGGICCTTGGCCAGGACGAAAGT 4770

-----G-----
ThrTrpSerLysIleArgAlaGlyLeuProIleSerProValAspLeuSerTyrLeuAlaProLysAsnProGlyThrGlyProAlaPhe

FIG.1N

HisProHisIleGlnAspAlaAlaSerGlnLeuProAspAspGluSerLeuPhePheGlyAspThrGlyLeuSerLysAsnProIleGlu

FIG. 10

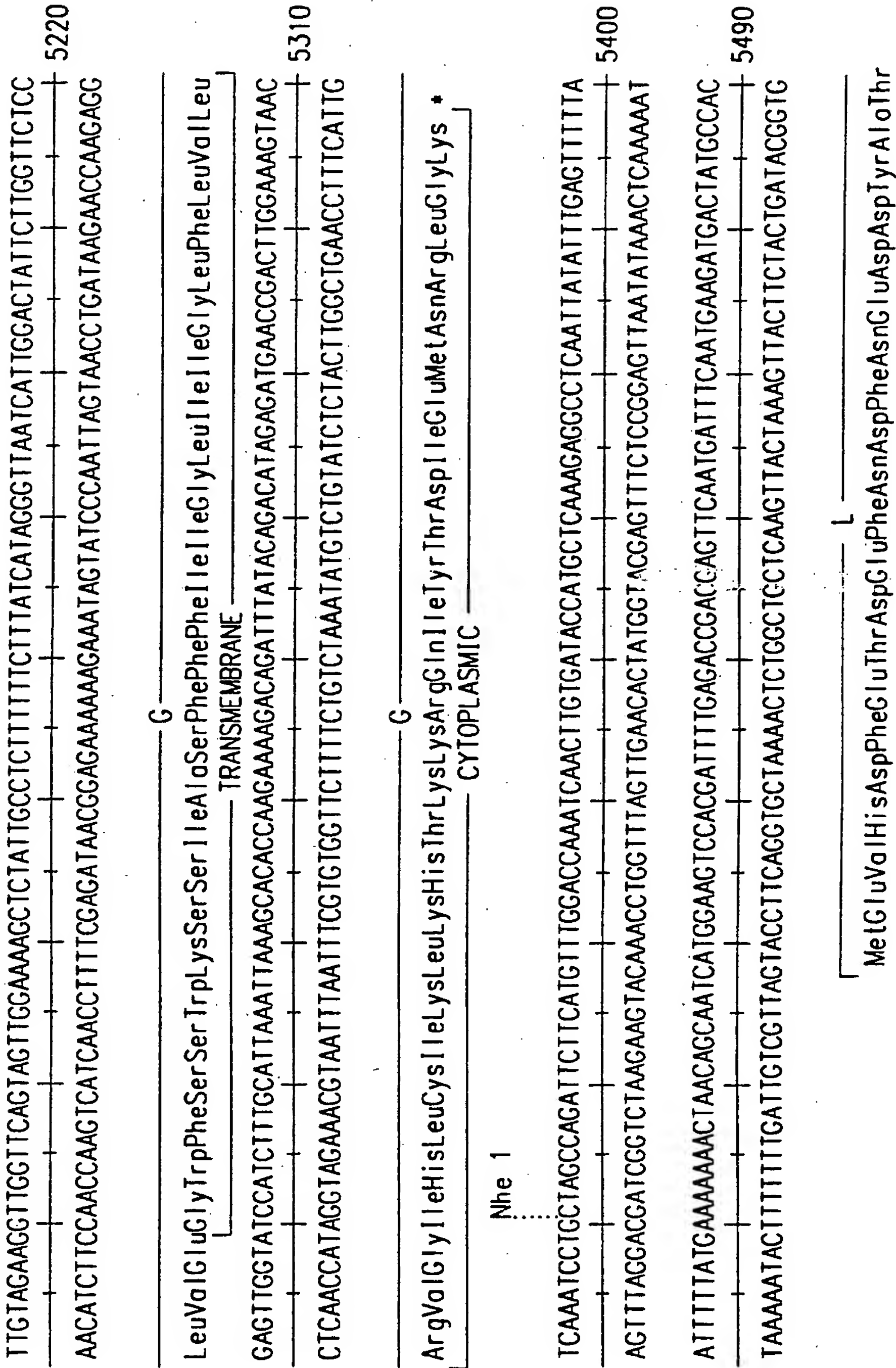


FIG.1P

ArgGluPheLeuAsnProAspGluArgMetThrTyrLeuAsnHisAlaAspTyrAsnLeuAsnSerProLeuIleSerAspAspIleAsp

AsnLeuIleArgLysPheAsnSerLeuProIleProSerMetTrpAspSerLysAsnTrpAspGlyValLeuGluMetLeuThrSerCys

GlnAlaAsnProIleSerThrSerGlnMetHisLysTrpMetGlySerTrpLeuMetSerAspAsnHisAspAlaSerGlnGlyTyrSer

FIG. 1Q

Sac 11

TTTTTACATGAAGTGCACAAAGAGCGCAGAAATAACATTTGACGTGGTGGAGACCTTCATCCGGCGCTGGGGCAACAAACCAATTGAATA
5850
AAAAATGTACTTACCTCGTTTCICCGICITTTATGTAACTGCACCACCTCTGGAAGTAGGGCCGACCCCGTTGTTGGTTAACITAT

PhelLeuHisGluValAspLysGluAlaGluIleThrPheAspValValGluThrPheIleArgGlyTrpGlyAsnLysProIleGluTyr

CATCAAAAAGGAAAGATGGACTGACTCATTCAAAATTCCTCGCTTATTTGTGTCAAAAGTTTTTGGACTTACACAAGTTGACATTAAATCTT
5940
GTAGTTTTTCCCTTTCTACCTGACTGACTAGTAACTTTAAGAGCGGAATAAACACAGTTTTCAAAACCCTGAATGTGTCAACTGTAAATTAGAA

IleLysLysGluArgTrpThrAspSerPheLysIleLeuAlaTyrLeuCysGlnLysPheLeuAspLeuHisLysLeuThrLeuIleLeu

AAATGCTGCTCTGAGGTGGAATTGCTCAACTTGGCGAGGACITTCAAAGCGCAAAGTCAGAAGAAGTTCTCAICGAACCAACATATGCAG
6030
TTTACGACAGACTCCACCTTAACGAGTTGAACCGCTCCTGAAAGTTTCCGTTTCAGTCTTCTCAAGAGTACCTTGCTTGATACGTC

AsnAlaValSerGluValGluLeuLeuAsnLeuAlaArgThrPheLysGlyLysValArgArgSerSerHisGlyThrAsnIleCysArg

GATTAGGTTCCAGCTTGGTCCCTACTTTTATTCAGAAGGATGGCTTACTTCAGAAACTTIGATATCTAATGGACCGAAACTTTCT
6120
CTAATCCCAAGGTCCGAACCCAGGATGAATAAAGTCTTCTACCCGAATGAAGTCTTTGAACIATAAGATTACCTGGCTTIGAAAGA

IleArgValProSerLeuGlyProThrPheIleSerGluGlyTrpAlaTyrPheLysLysLeuAspIleLeuMetAspArgAsnPheLeu

FIG.1R

GTAA TGGTCAAAGA TGA TATAGGAGGATGCAAACGGTGCATCCATGGTATGTAGAAATAGACAACCTGTCTCTCAGAGCAAGACAT
 CAATTACCAGTTTCTACACTAAATATCCCTCCCTACGTTGCCACGATAGGTACCATACATCTTATCIGTTGGACAAGAGICTCGTTCTGTGA 6210

LeuMetValLysAspValIleIleGlyArgMetGlnThrValLeuSerMetValCysArgIleAspAsnLeuPheSerGluGlnAspIle

CTTCTCCCTTCTAAATACTACAGAAATGGAGATAAAATGTGGAGAGCCAGGGAATTTTCTTAIGACTTGAATTAATAIGGTGGAACC
 GAAGAGGGAAGATTTATAGATGCTTAACCTCTATTTTAACACCCTCCGTCCTTTTAAAGAATACTGAACCTAATTTTACCACCTTGG 6300

PheSerLeuLeuAsnIleTyrArgIleGlyAspLysIleValGluArgGlnGlysnPheSerTyrAspLeuIleLysMetValGluPro

GATATGCAACTTGAAGCTGATGAATTAGCAAGAGAAATCAAGGCCTTTAGTCCCAACAATCCCTCATTTTGAATAATCATATCAAGACTTC
 CTATACGTTGAACCTCCGACTACTTAAATCGTTCTCTTAGTTCGGAAATCAGGGGTGTTAAGGGAGTAAAACTTTTAGTATAGTCTCTGAAG 6390

IleCysAsnLeuLysLeuMetLysLeuAlaArgGluSerArgProLeuValProGlnPheProHisPheGluAsnHisIleLysThrSer

TGTTGATGAAGGGGCAAAAATGACCGAGGTATAAGATTCCTCCATGATCAGATAATGAGTGTGAAACAGTGGATCTCACACITGGTGAT
 ACAACTACTTCCCGGTTTTAACTGGCTCCATATCTAAGCAGGTACTAGTCTATTACICACACTTTTGTACCTAGAGTGTGACCACCTA 6480

ValAspGluGlyAlaLysIleAspArgGlyIleArgPheLeuHisAspGlnIleMetSerValLysThrValAspLeuThrLeuValIle

FIG.1S

20/50

TTATGGATCGTTCAGACATTCGGGTCAICCTTTTATAGATTATTACACTGGACTAGAAAAATTACATTCCCAAGTAACCAAGAAGA
 AATACCTAGCAAGTCTGTAACCCAGTAGGAAAAATATCTAATAAIGTGACCIGATCTTTTAAATGAAGGTTCAATGGTACTTCTTCT 6570

TyrGlySerPheArgHisTrpGlyHisProPheIleAspTyrTyrThrGlyLeuGluLysLeuHisSerGlnValThrMetLysLysAsp

TATTCATGTCATATGCAAAAGCACTTCGAAGTGATTTAGCTCCGATTGTCTTATTTCAACAGTTCAATGATCATAAAAAGTGGTTCGT
 ATAACCTACACAGTATACGTTTTCGTCAACGTTCACTAAATCGAGCCTAACACAGATAAAGTTGTCAGTTACTAGTATTTTTCACCAAGCA 6660

IleAspValSerTyrAlaLysAlaLeuAlaSerAspLeuAlaArgIleValLeuPheGlnGlnPheAsnAspHisLysLysTrpPheVal

GATGGAGACTTGCCTCCTCATGATCATCCCTTTAAAGTCATGTTAAAGAAAAATACATGGCCACAGCTGCTCAAGTTCAAGATTTTGG
 CTTACCTCTGAACGAGGAGTACTAGTAGGAAATTTTCAGTACAATTTCTTTTAATGACCGGTCGACGAGTTCAAGTTCTAAAAACC 6750

AsnGlyAspLeuLeuProHisAspHisProPheLysSerHisValLysGluAsnThrTrpProThrAlaAlaGlnValGlnAspPheGly

AGATAAATGGCAAGCACTTCCCTGATTAATGTTTGAATATACCCGACTTACTAGACCCATCGATAATACTCTGACAAAAAGTCATTC
 TCTATTTACCGTACTTGAAGCGGCACTAATTTACAAAACCTTTATCGGCTGAATGACCTGGTAGCTATTATATGAGACTGTTTTCAGTAAG 6840

AspLysTrpHisGluLeuProLeuIleLysCysPheGluIleProAspLeuLeuAspProSerIleIleTyrSerAspLysSerHisSer

FIG.1T

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AAATGAATAGGTCAGAGGTGTGAAACAATGTCGGAATGAATCCGAACACICCTATCCCTAGTAAAGGIGTTCAGACIATGTTGGACAC
TTACTTATCCAGTCICCAACACTTGTACAGGCTTACTTAGGCTGTGAGGATAGGATCATTTTCCACAACGICTGATACAACCTGIG 6930

MetAsnArgSerGluValLeuLysHisValArgMetAsnProAsnThrProIleProSerLysLysValLeuGlnThrMetLeuAspThr

AAAGGCTACCAATTGGAAAGAATTTCITTAAGAGAGATGATGAGAAGGCGCTTAGATGATGATCATAATTATGGTCTTAAAGGAAAGGA
TTTCCGATGGTTAACCCTTCTTAAAGAATTTCICTAACTACTCTTCCCGAATCTACTACTAGATTATAAACCAGAAATTCCTTTCCCT 7020

LysAlaThrAsnTrpLysGluPheLeuLysGluIleAspGluLysGlyLeuAspAspAspLeuIleIleGlyLeuLysGlyLysGlu

GAGGAACTGAAGTTCGCAGGTAGATTTTCTCCCTAAATGCTCTGGAAATTCGCAATACTTTGTAAATTACCGAATATTIGATAAAGAC
CTCCCTTGACTTCAACCGTCCATCTAAAAGAGCGGATTACAGAACCCTTAACGCTCTTATGAACACATTAAATGGCTTATAAACAATTCTCTG 7110

ArgGluLeuLysLeuAlaGlyArgPhePheSerLeuMetSerTrpLysLeuArgGluTyrPheValIleThrGluTyrLeuIleLysThr

TCATTTGCTCCCTATGTTTAAAGCCCTGACAAATGCGCGACGATCTAACTGCAGTCATTAAAAAGATGTTAGATTCCCTCATCCGGCCCAAGG
AGTAAAGCAGGGATACAAATTTCCGGACTGTACCGCCTGTAGATTGACGTCAGTAAATTTTCTACAATCTAAGGAGTAGGCCGGTTCC 7200

HisPheValProMetPheLysGlyLeuThrMetAlaAspAspLeuThrAlaValIleLysLysMetLeuAspSerSerSerGlyGlnGly

FIG.1U

ATTGAAGTCATATGAGGCAATTTCATAGCCAAATCACAATGATTACGAAAAATGCAATAACCCACCAAGGAAGTTATCAAAACGGCCACAGT
 TAACTTCAGTATACTCCGTTAAACGTAICGGTATAGTGAATGCTTTTACCTTATIGGTGCTTCCITCAATAGTTGCCCGGTCA 7290

LeuLysSerTyrGluAlaIleCysIleAlaAsnHisIleAspTyrGluLysTrpAsnAsnHisGlnArgLysLeuSerAsnGlyProVal

GTTCCGAGTTATGGGCCAGTTCTTAGGTATCCATCCTTAATCGAGAGAACTCAATGATTTTGTGAGAAAGTCTTATATACTACAATGG
 CAAGGCTCAATACCCGGTCAAGAAATCCAATAGGTAGGAATTAGCTCTCTTGAGTACTTAAAAAACICTTTICAGAAATATAIGATGTTACC 7380

PheArgValMetGlyGlnPheLeuGlyTyrProSerLeuIleGluArgThrHisGluPhePheGluLysSerLeuIleTyrTyrAsnGly

AAGACCAGACTTGAATGCGTTCACAAACACACATGATCAATTCACCTCCCAACGAGTTTGTGGCAAGGACAGAGGGTGGACTGGA
 TTCTGGTCTGAACACGACAAAGTGTGTGTGTGACTAGTTAAGTTGGAGGTTGCICAAACACCGTTCCCTGTCTCCACCTGACCT 7470

ArgProAspLeuMetArgValHisAsnAsnThrLeuIleAsnSerThrSerGlnArgValCysTrpGlnGlyGlnGlyLeuGlu

AGGCTACGGCAAAAGGATGGACTATCTCTCAATCTACTGGTTATTCAAAGAGAGGCTAAAAATCAGAAACACACCTGCTCAAAAGTCTTGGC
 TCCAGATGCCGTTTTTCCCTACCTGATAGGAGTTAGATGACCAATAAGTTCTCTCCGATTTAGCTTTGTGACGACAGTTTCAGAAACCG 7560

GlyLeuArgGlnLysGlyTrpThrIleLeuAsnLeuLeuValIleGlnArgGluAlaLysIleArgAsnThrAlaValLysValLeuAla

FIG.1V

ACAAGGTGATATAAACAAGTATTAACGAGAAATCGAGAACCTTGTAATACAGGGTCTCTCAATCAAATGGT
 TGTCCACTATTAGTTCAATAAAGGTGIGTCAATTTTGCTTCTTAGCTCTTTGCAACATCTTAATGTCCACGAGAGTTAGTTTACCA 7650

GlnGlyAspAsnGlnValIleCysThrGlnTyrLysThrLysLysSerArgAsnValValGluLeuGlnGlyAlaLeuAsnGlnMetVal

TTCTAATAAGAGAAATTAAGACTGCAATCAAAATAGGGACAGGGAAGTTAGGACTTTTGATAAATGACGATGAGACTAIGCAATCTGC
 AAGATTATTACTCTTTTAATACTGACGTTAGTTTATCCCTGTCCTTCAATCCGAAACIATTTACTGCTACICTGATACGTTAGACG 7740

SerAsnAsnGluLysIleMetThrAlaIleLysIleGlyThrGlyLysLeuGlyLeuLeuIleAsnAspAspGluThrMetGlnSerAla

AGATTACTTGAATTATCGAAAAATACCGATTTCCGTGGAGTGATTAGACGGTTAAGACCAAGAGATGGTACGAGTGTGTCAC
 TCTAATGAACCTTAATACCTTTTAIGGCTAAAGGCCCTCACTAATCTCCCAATCTCTGTTCTCTACCGAGTGTCTACGACACACAGTG 7830

AspTyrLeuAsnTyrGlyLysIleProIlePheArgGlyValIleArgGlyLeuGluThrLysArgTrpSerArgValThrCysValThr

FIG.1W

Sac 1

CAATGACCAAAATACCCACTTGTGCTAAATATAATGAGCTCAGTTTCCACAAATGCCTCTCACCCTAGCTCATTTTGGCTGAGAACCCCAATCAA
GTTACTGGTTTATGGGTGAACACCGATTATATTACTCGAGTCAAAGGTGTTTACGAGAGTGGCAATCGAGTAAACCGACCTCTTGGCTTAGTT 7920

AsnAspGlnIleProThrCysAlaAsnIleMetSerSerValSerThrAsnAlaLeuThrValAlaHisPheAlaGluAsnProIleAsn

TGCCATGATACAGTACAATTATTTGGGACATTTGGTAGACTCTTGTGATGATGCAATCCCTGCTCTTGGTCAATCATTTGTAAGAAT
ACGGTACTATGTCATGTTAATAAAACCCGTGTAACGATCTGAGAACAACTACTACGTACTAGGACGAGAACGAGTTAGTAACATACTTCA 8010

AlaMetIleGlnTyrAsnTyrPheGlyThrPheAlaArgLeuLeuMetMetHisAspProAlaLeuArgGlnSerLeuTyrGluVal

TCAAGATAAGATAACCGGCTTGCACAGTCTACTTTCAAATACGCCATGTGTATTTGGACCCCTTCCATTGGAGGAGTGTGGGCGCATGTC
AGTTCTATTCTATGCCCGGAACGGTGTCAGATGAAAGTTTATCGGGTACAACATAAACCTGGGAAGTTAACCTCCTCACAGCCCGTACAG 8100

GlnAspLysIleProGlyLeuHisSerSerThrPheLysTyrAlaMetLeuTyrLeuAspProSerIleGlyGlyValSerGlyMetSer

FIG.1X

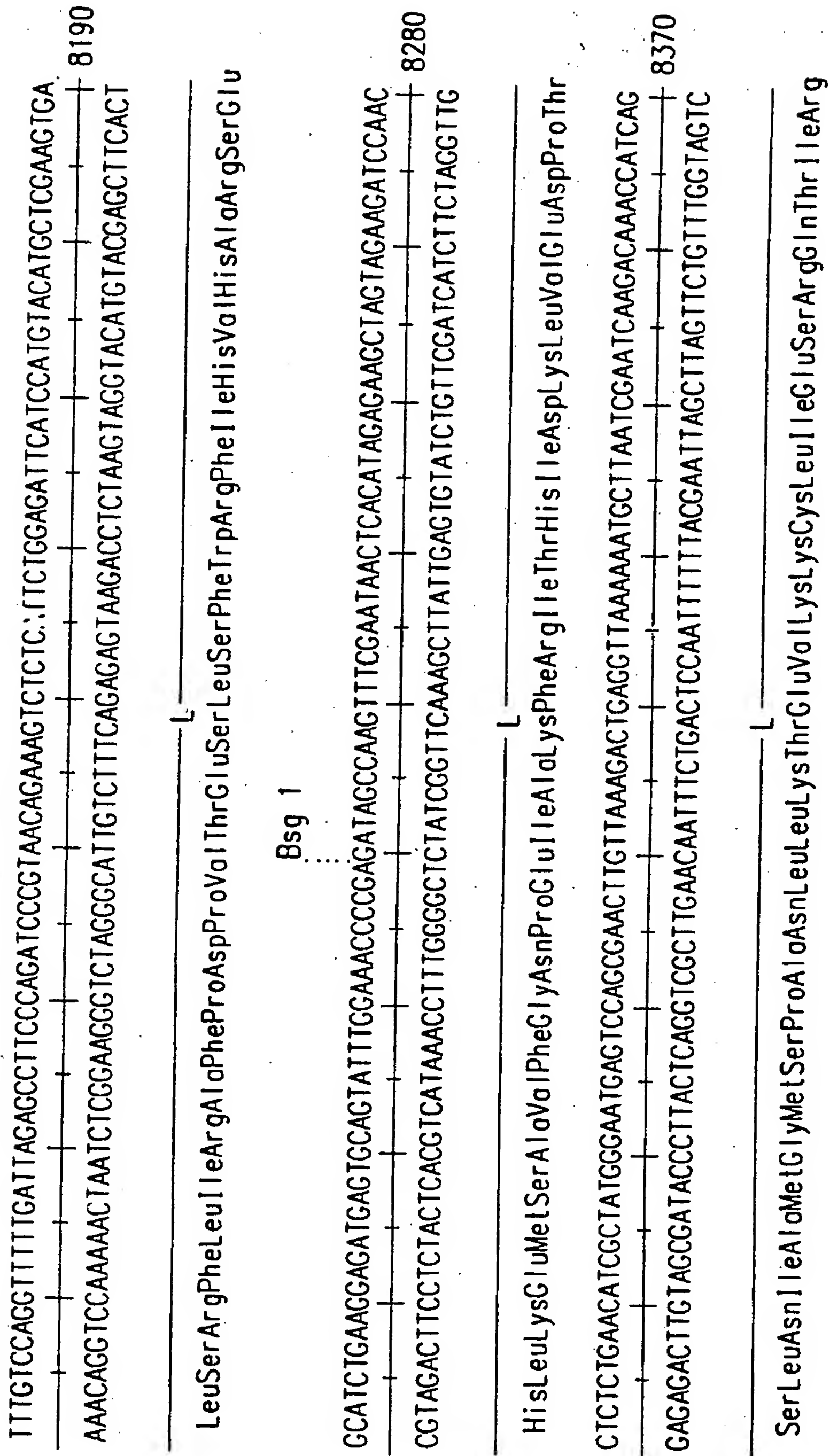


FIG.1Y

GAACCAGGTGATTAAAGGATGCAACCATATATTGTATCATGAAGAGGATCGGCTCAGAAGTTCTTATGGTCAATAAAATCCTCTGTTCCC
CTTGGTCCACTAATTCCTACGTGGTATATAAACAATAGTACTTCICCTAGCCGAGTCTTCAAAGAAATACCAGTTATTTAGGAGACAAGGG 8460

AsnGlnValIleLysAspAlaThrIleTyrLeuTyrHisGluGluAspArgLeuArgSerPheLeuTrpSerIleAsnProLeuPhePro

TAGATTTTAAAGTGAATTCAAATCAGGCACCTTTTGGAGTCCAGACGGCTCATCAGICTATTTCAAATTCCTCGTACTATTCGGAA
ATCTAAAAATTCACCTTAAGTTAGTCCGTGAAAAACCCCTCAGCGTCTGCCGAGTAGTCAGATAAAGTTTAAAGACCATGATAAGCCTT 8550

ArgPheLeuSerGluPheLysSerGlyThrPheLeuGlyValAlaAspGlyLeuIleSerLeuPheGlnAsnSerArgThrIleArgAsp

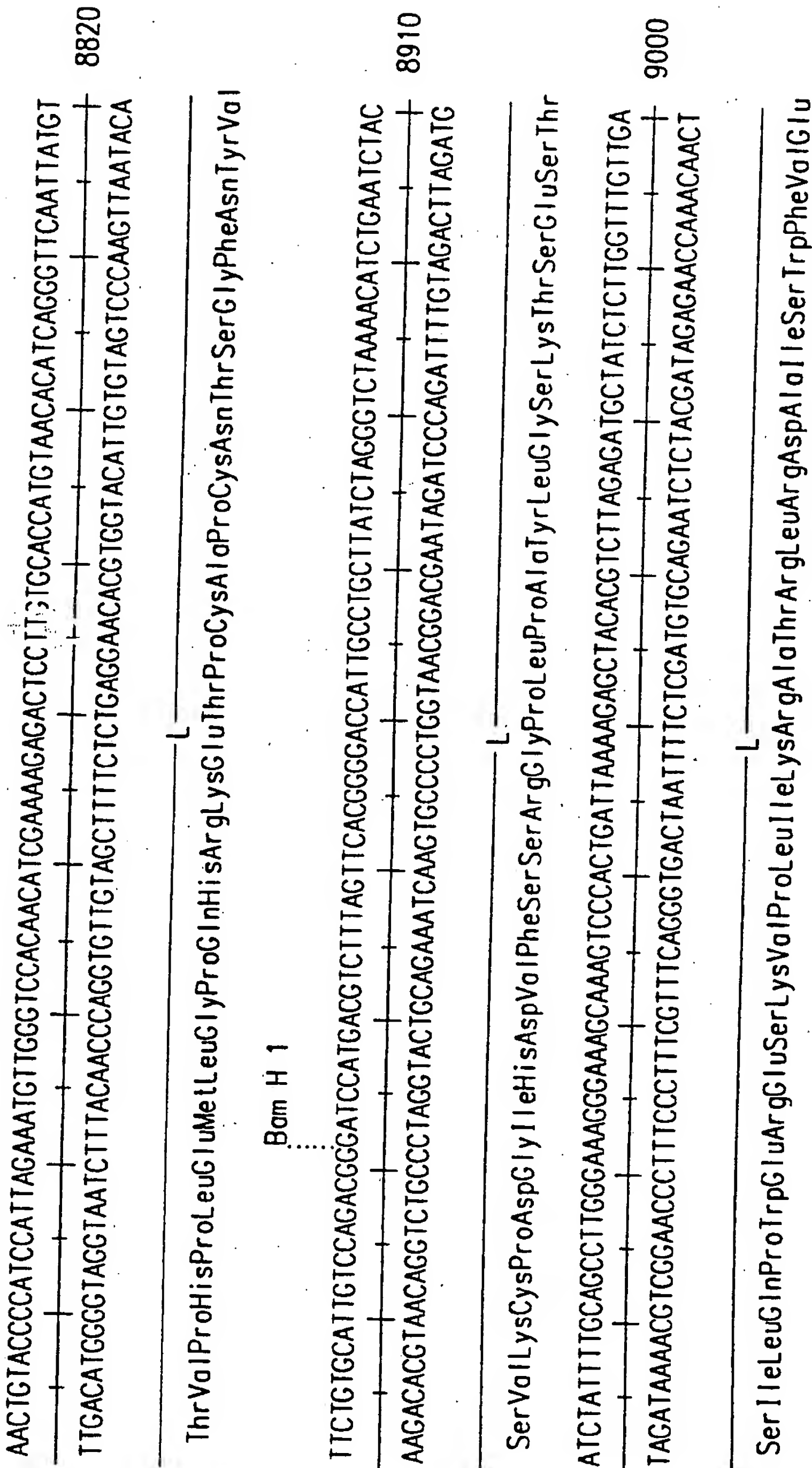
CTCCTTTAAGAAAAAGTATCATAGGGAATTGGATGATTGATGTGAGGAGTGGTATCCCTTTGACACATTTAGGGAACCTTCATTT
GAGGAAATTCCTTTTCATAGTATCCCTTAACCTACTAACTAACACCTCCTCCTCATAGGAGAAACIGTGTAATCCCTTIGAAGTAAA 8640

SerPheLysLysLysTyrHisArgGluLeuAspAspLeuIleValArgSerGluValSerSerLeuThrHisLeuGlyLysLeuHisLeu

GAGAGGGGATCATGTAAAAATGGACATGTTCAGCTACTCATCTGACACATTAAGATACAAATCCTCGGCCGTACAGTTATTGGGAC
CTCTTCCCCCTAGTACATTTACACCCTGTACAAGTCGATCAGTACGACCTGTAAATCTATGTTTAGGACCCCGGCATGTCATAACCCCTG 8730

ArgArgGlySerCysLysMetTrpThrCysSerAlaThrHisAlaAspThrLeuArgTyrLysSerTrpGlyArgThrValIleGlyThr

FIG.1Z



Bam H 1

FIG.1A1

ACCCGACTCTAAACTAGCAATGACTATACTTTCTAACAATCCACATCTTTAACAGGGCGAAGAAATGGACCAAAAGGCAGCATGGGTTCAAAAG
 TGGCGTGAAGATTGATCGTTACTGATATGAAGATGTAGGTGAGAAATTGTCGGTTCTTACCTGGTTTCCGTCGTACCCCAAGTTTTC 9090

ProAspSerLysLeuAlaMetThrIleLeuSerAsnIleHisSerLeuThrGlyGluGluTrpThrLysArgGlnHisGlyPheLysArg

AACAGGGTCIGCCCTTCATAGGTTTTCGACATCTCGGATCAGCCATGGTGGTTCGCAATCTCAGAGCACATGCAGCATTGACCAGGTTCAT
 TTGTCACAGACGGGAAGTATCCAAAGCTGTAGAGCCCTACTCCGTACCAACCAAGCGTAGAGTCTCGTGACGTGCTAACCTGGTCCAACCTA 9180

ThrGlySerAlaLeuHisArgPheSerThrSerArgMetSerHisGlyGlyPheAlaSerGlnSerThrAlaAlaLeuThrArgLeuMet

GGCAACTACAGACACCAATCAGCGATCTGGGAGATCAGAAATTCGACTTTTATTCGAAGCAACGTTCCTCTATGCICAAATTACCACCAC
 CCGTTGATGTCGTGGTACTCCCTAGACCCCTCTAGTCTTAAAGCTGAAAAATAGGTTCCGTTCGAACGAGATACGAGTTTAAATGGTGGTG 9270

AlaThrThrAspThrMetArgAspLeuGlyAspGlnAsnPheAspPheLeuPheGlnAlaThrLeuLeuTyrAlaGlnIleThrThrThr

TGTTCGAAGACAGACCGATCGATCACCAGTTGTACAGATCATATCAATATGCCCTGTAAGTCCCTGTTGAGACCCATAGAAGAGATCACCCCT
 ACAACGTTCCTGCTACCTAGTGGTCAACATGTCTAGTATAGTATAACCGACATTCAGGACAAACCTCGGTATCTCTCTAGTGGGA 9360

ValAlaArgAspGlyTrpIleThrSerCysThrAspHisTyrHisIleAlaCysLysSerCysLeuArgProIleGluGluIleThrLeu

FIG.1B1

9450

GGACTCAAGTATGGACTACACGCCCCCAGATGTCCTGAAGACATGG.IGGAATGGGGAAGGTTCTGGGGACAAGAGATAAA
CCTGAGTTTCAATACCTGATGTCGGGGGGTCTACATAGGGTACACGACTTCTGTATC.CCTTACCCCTTCCAAGCACCCCTGTTCTCTATTT

L

AspSerSerMetAspTyrThrProProAspValSerHisValLeuLysThrTrpArgAsnGlyGluGlySerTrpGlyGlnGluIleLys

9540

ACAGATCTATCCTTTAGAAGGGAATTGGAAGAAATTAGCACCTGCTGAGCAAICCTATCAAGTCGGCAGATGATAGGTTTTCIATAIGG
TGCTAGATAGGAAATCTTCCCTTAACCTTCTTAAATCGTGGACGACICGTTAGGATAGTTACGCCGCTCATAATCCAAAGATATACC

L

GlnIleTyrProLeuGluGlyAsnTrpLysAsnLeuAlaProAlaGluGlnSerTyrGlnValGlyArgCysIleGlyPheLeuTyrGly

9630

AGACTTCGGGTATAGAAAICTACTCATGCCGAGGACAGTTCTCTATTTCCTCTATCTATACAAGTCGTTATAGAGTCGAGGTTTCTT
TCTGAACCCGCATATCTTTTAGATGAGTACGCCCTCCTGTCAAGAGATAAAGGAGATAGATAATGTTCCAGCATAAICTCCAGCTCCCAAAGAA

L

AspLeuAlaTyrArgLysSerThrHisAlaGluAspSerSerLeuPheProLeuSerIleGlnGlyArgIleArgGlyArgGlyPheLeu

FIG.1C1

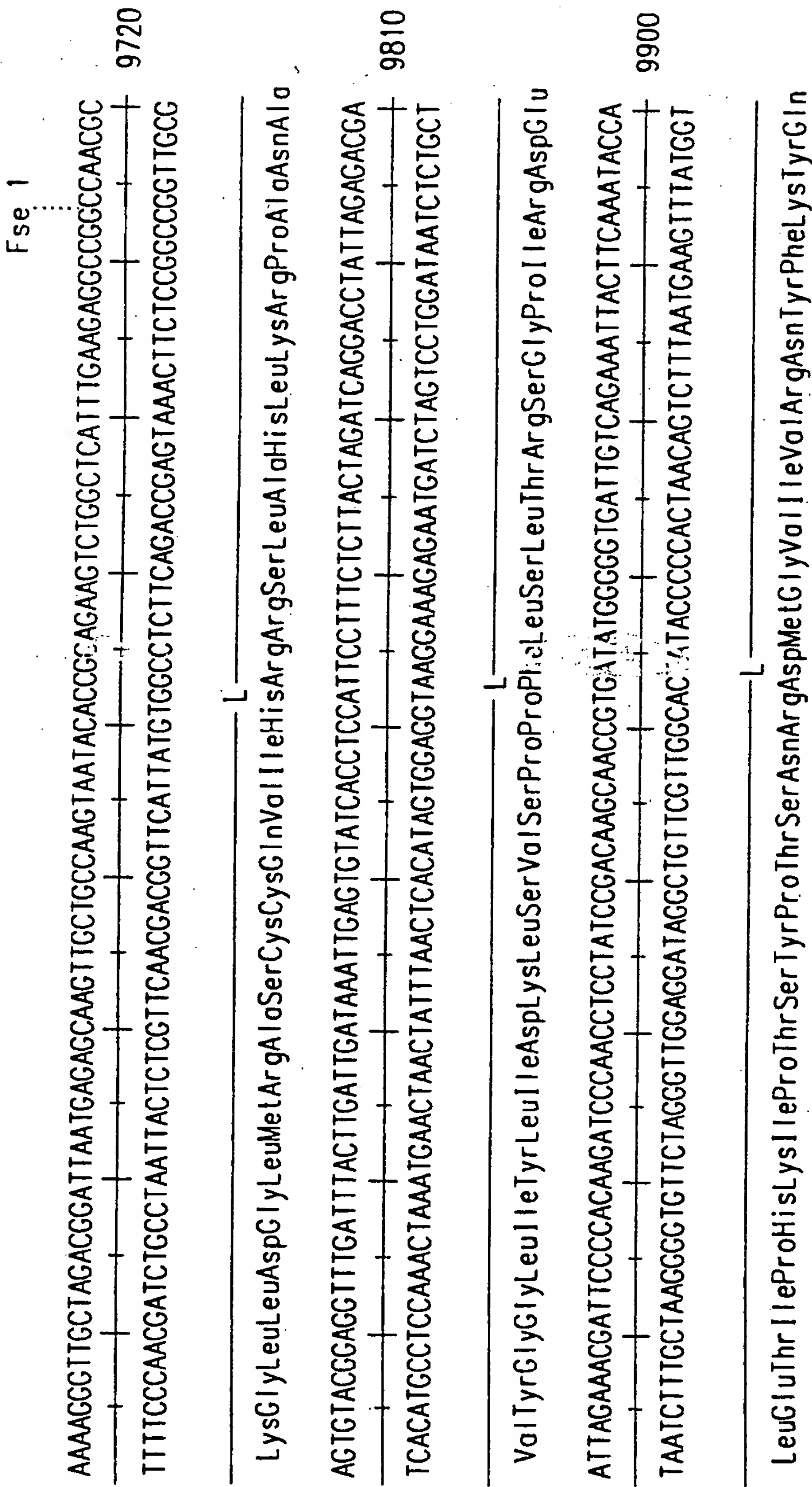


FIG.1D1

ATCCCGTCTAATTGAAAAGCGAAAAATACAGATCACAATTATTCACAATTATTCAGATGCTCTTATCCATAGACITTCATTGGACC
TACGGCAGATTAACTTTTCCCTTTTATGCTCTAGTGTAAATAAGTGTAAATACCAA⁹⁹⁹⁰TAAGAGTCTACAGAAATAGGTATCTGAAGTAACCTGG

L
CysArgLeuIleGluLysGlyLysTyrArgSerHisTyrSerGlnLeuTrpLeuPheSerAspValLeuSerIleAspPheIleGlyPro
ATTCTCTATTCCACCACCCCTCTTCGCAATCCCTATACAAGCCATTTTATCTCGGAAGATAAGAATGAGTTGAGAGAGCTGGCAAATCT
TAAGACATAAAGGTGGTCGGAGAACGTTTAGGATAGTTCGGTAAAAATAGACCCCTTCTATCTTACTCAACICCTCGACCGTTTAGA¹⁰⁰⁸⁰

L
PheSerIleSerThrThrLeuleuGlnIleLeuTyrLysProPheLeuSerGlyLysAspLysAsnGluLeuArgGluLeuAlaAsnLeu
TTCTTCATTGCTAAGATCAGGAGAGGGTGGGAAGACATACATGIGAAATCTTCACCAAGGAGATATTATGTGTCAGAGGAAATCAG
AAGAAGTAACGATTCTAGTCTCTCCCCACCCCTTCGTGTACACTTAAGAAGTGTTCCTGTATATAACACAGGTCCTCTTATGTC¹⁰¹⁷⁰

L
SerSerLeuLeuArgSerGlyGluGlyTrpGluAspIleHisValLysPhePheThrLysAspIleLeuLeuCysProGluGluIleArg
ACATGCTTCCAAGTTCGGGATTGCTAAGGATAATAATAAGACATGAGCTATCCCCCTTCGGGAAGGGAATCCAGAGGACAATTACAAC
TGTAACGAACGTTCAAGCCCTAACGATTCCTATTATTTCGTACTCGATAGGGGAACCCCTTCCCTTAGGTCCTCCCTGTTAATGTTG¹⁰²⁶⁰

L
HisAlaCysLysPheGlyIleAlaLysAspAsnLysAspMetSerTyrProProTrpGlyArgGluSerArgGlyThrIleThrThr

FIG.1E1

ATCCCTGTTTATTACGACCACCCCTTACCCAAAGATGCTAGAGATGCCCTCCAGAAATCCAAATCCCTGCTGCCGGAATCAGGTT
TTAGGACAAATAATATGCTGGTGGGAATGGTTTCTACGATCTCTACGGAGGTCTTAGGTTTATAGGGACGACAGGCCCTTAGTCCAA 10350

-----L-----
IleProValTyrTyrThrThrProTyrProLysMetLeuGluMetProProArgIleGlnAsnProLeuLeuSerGlyIleArgLeu

GGCCCAATTACCAACTGCGGCTCATTAATAAAATCGGAGTATAATTACATGGAAATGGGAATCCATTACAGGGACTTCTTGAGTTGGGAGA
CCCGGTTAATGGTTGACCGCGAGTAATAATTTAAGCCTCATAATAATGTAACCTTACCCCTAGGTAATGTCCTGAAGAACTCAACACCTCT 10440

-----L-----
GlyGlnLeuProThrGlyAlaHisTyrLysIleArgSerIleLeuHisGlyMetGlyIleHisTyrArgAspPheLeuSerCysGlyAsp

CGGCTCCGGAGGATGACTGCTGCATTACTACGAGAAAATGTCATAGCAGAGGAATATTCATAGTCTGTTAGAAATTATCAGGGTCAGT
CGCGAGCCCTCCCTACTGACGACGTAATGATGCTCTTTTACACGTAICGTCICCTTATAAGTTATCAGACAAICTTAATAGTCCCAGTCA 10530

-----L-----
GlySerGlyGlyMetThrAlaAlaLeuLeuArgGluAsnValHisSerArgGlyIlePheAsnSerLeuLeuGluLeuSerGlySerVal

FIG.1F1

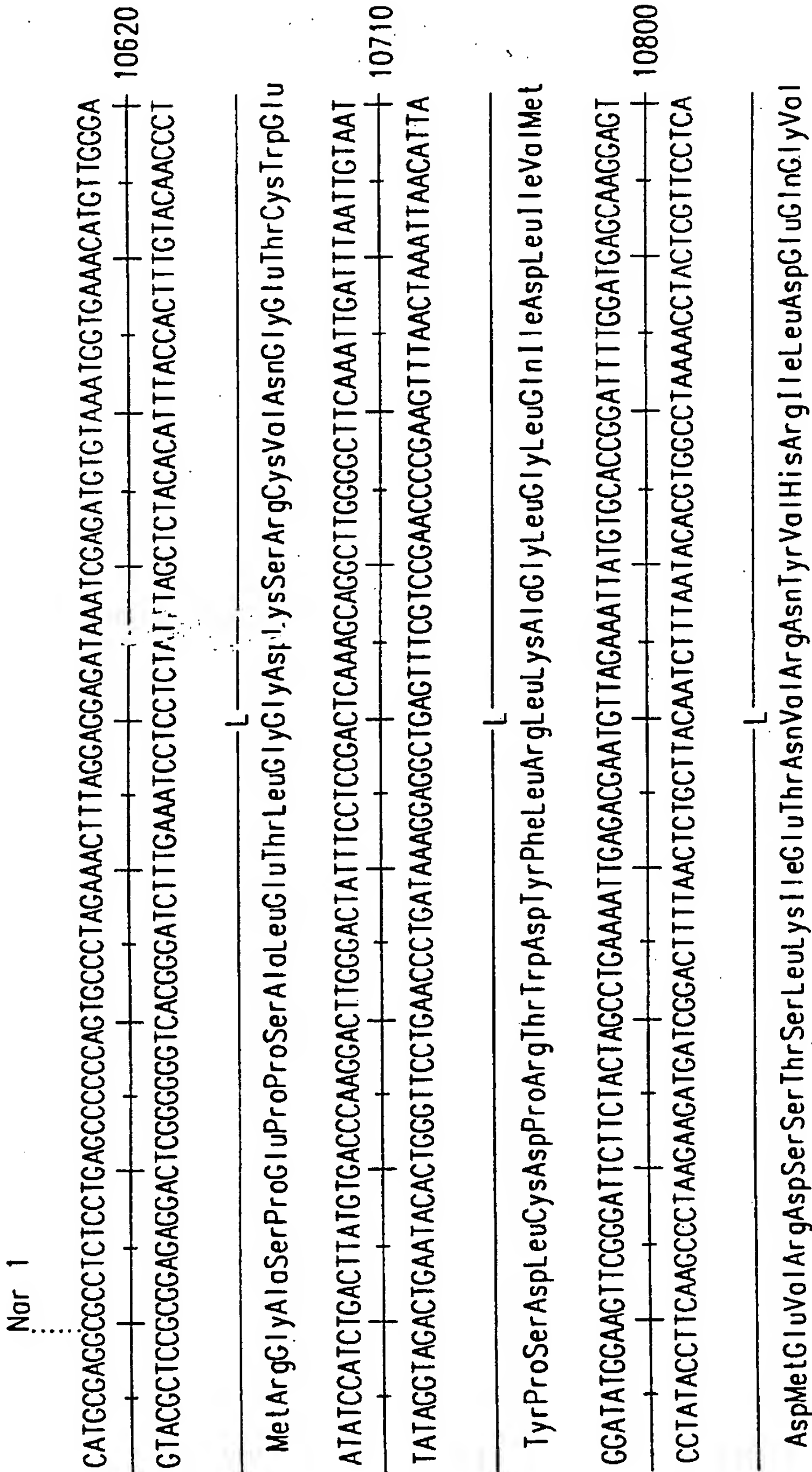


FIG.1G1

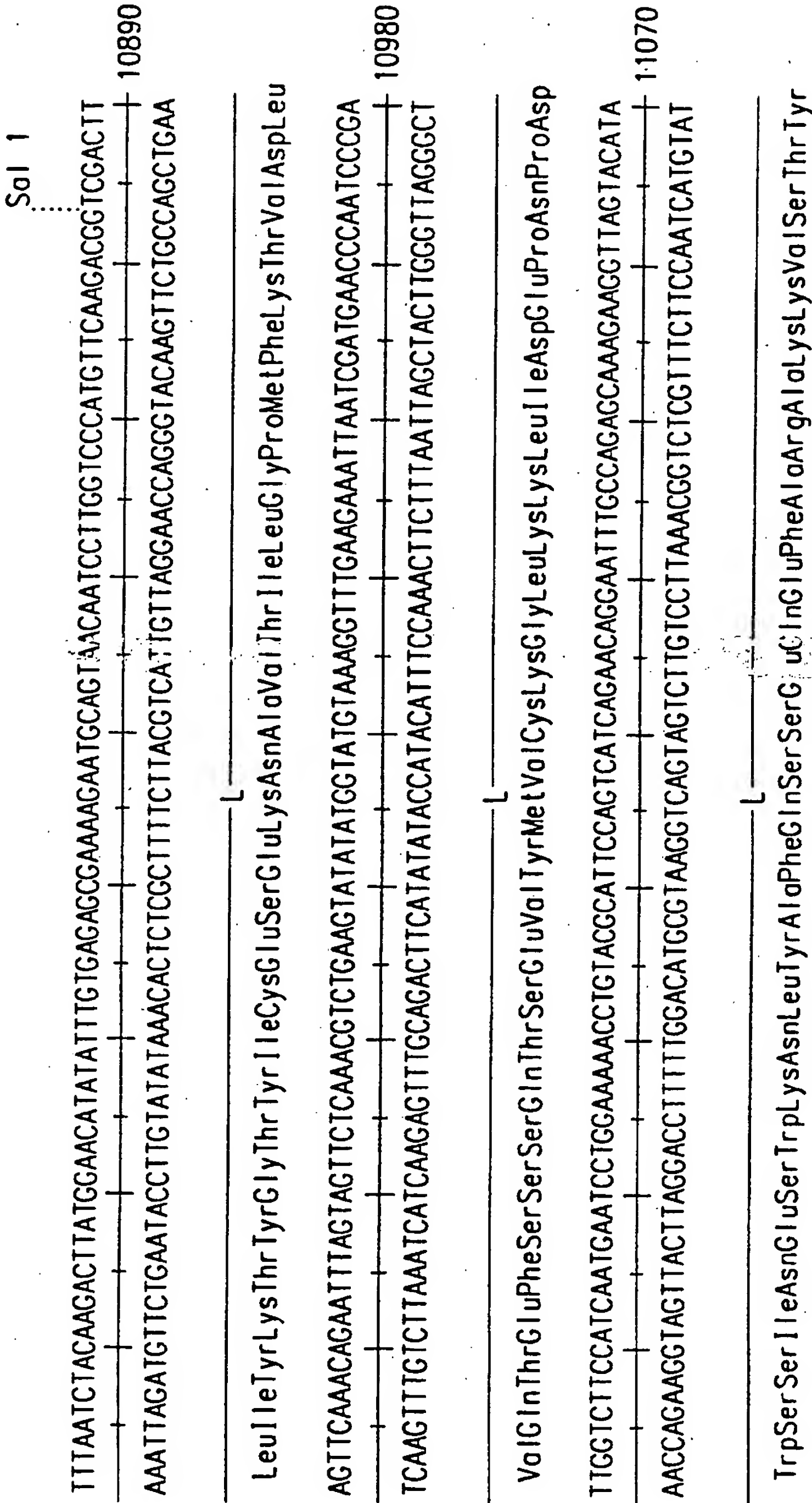


FIG. 1H1

C T T T A C C T T G A C A G G T A T T C C C T C C C A A T T C A T T C C T T T T G T A A C A T T G A G A C T A T G C T A C A A A T A T T C G G A G T A C C C A C G G G
G A A A T G G A A C T G T C C A T A A G G G A G G G T T A A G T A A G G A C T A G G A A A C A T T T G T A A C T C T G A T A C G A T G T T T A T A A G C C T C A T G G G T G C C C 11160

— L —
P h e T h r L e u T h r G l y I l e P r o S e r G l n P h e I l e P r o A s p P r o P h e V a l A s n I l e G l u T h r M e t L e u G l n I l e P h e G l y V a l P r o T h r G l y

T G T G T C T C A T G C G G C T G C C T T A A A A T C A T C I G A T A G A C C T G C A G A T T T A T T G A C C A T T A G C C T T T T T A T A T G G C G A T T A T A T C G T A T T A
A C A C A G A T A C G C C G A C G G A A T T T T A G T A G A C T A T C I G G A C G T C T A A A T A A C T G G T A A T C G G A A A A A T A T A C C G C T A A T A T A G C A T A A T 11250

— L —
V a l S e r H i s A l o A l o A l e u L y s S e r S e r A s p A r g P r o A l o A s p L e u L e u T h r I l e S e r L e u P h e T y r M e t A l o I l e I l e S e r T y r T y r

T A A C A T C A A T C A T A T C A G A G T A G G A C C G A T A C C T C C G A A C C C C C C A T C A G A T G G A A T T G C A C A A A A T G T G G G A T C G C T A T A A C T G G T A T
A T T G T A G T T A G T A T A G T C T C A T C C T G G C T A T G G A G G C T T G G G G G T A G T C T A C C T T A A C G T G T T T T A C A C C C C C T A G C G A T A T T G A C C A T A 11340

— L —
A s n I l e A s n H i s I l e A r g V a l G l y P r o I l e P r o P r o A s n P r o P r o S e r A s p G l y I l e A l o G l n A s n V a l G l y I l e A l o I l e T h r G l y I l e

FIG.111

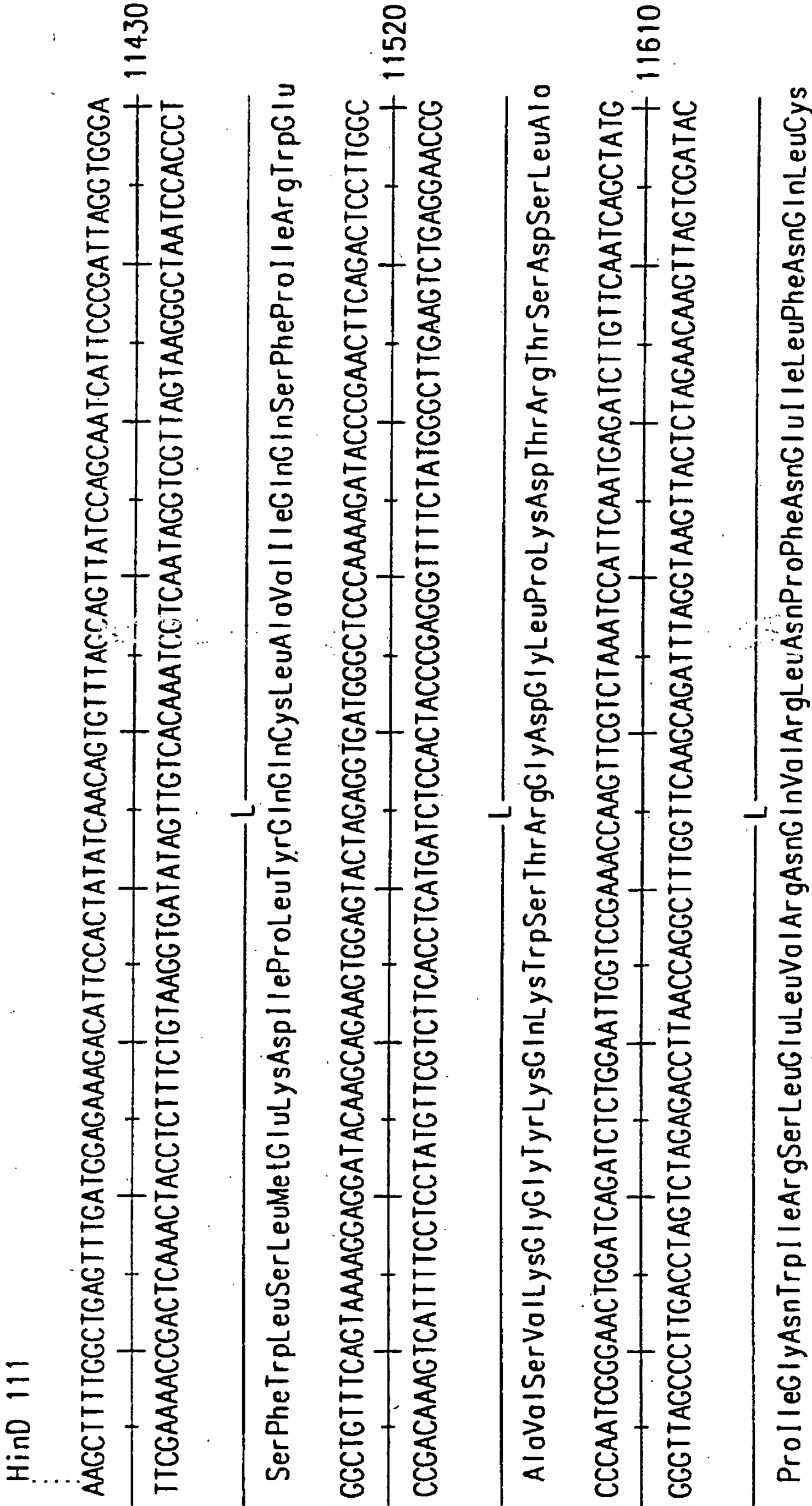


FIG. 1J1

TCGTACAGTCGATAATCATTTGAAATGGTCAAATTTCCGAAGAAACACAGCAATGATTGAATCGATCAATAGACCAATTTCAAAGAAGA
AGCATGTCACCTATTAGTAAACTTTACCAGTTTAAACGCTTCTTTGIGTCCTTACTAACTTACCTAGTTAICTGCTTAAAGTTTCTTCT

11700

ArgThrValAspAsnHisLeuLysTrpSerAsnLeuArgArgAsnThrGlyMetIleGluTrpIleAsnArgArgIleSerLysGluAsp

CCGGTCTATACIGATGTTGAAGAGTGACCTACACGAGGAAACICTTGGAGAGATTAAAAATCAIGAGGAGACITCCAAACTTTAAGTAT
GGCCAGATATGACTACAACTTCTCAGTCGATGTCCTCTTTTGAGAACCCTCTCTATTTTATTAGTACTCCTCTGAGGTTTGAAATTCATA

11790

ArgSerIleLeuMetLeuLysSerAspLeuHisGluGluAsnSerTrpArgAsp *

Ala 11

GAAAAAACTTTGATCCTTAAGACCCCTTGTGGTTTTTATTTTATCIGGTTTGTGGTCTTGGTGGGTCGGCATGCCATCACCCT
CTTTTTTGAACCTAGGAATCTGGGAGAACACCAAAAAATAAAAAATAGACCAAAACACCAGCACCCAGCCGTACCCGTAGAGGTGGA

11880

RBZ

CCTCGCCGTCCGACCTCGGCATCCGAAGGAGGACGTGCTCCACTCGGATGGCTAAGGGAGGGGCCCCCGGGGGCTGCTAACAAAGCCCG
GGACGCCAGGCTGGACCCGTAGGCTTCTTCGACGAGGTGAGCCTACCGATTCCCTCCCGGGGGGGCCCGACCATGTTCGGGGC

11970

FIG. 1K1

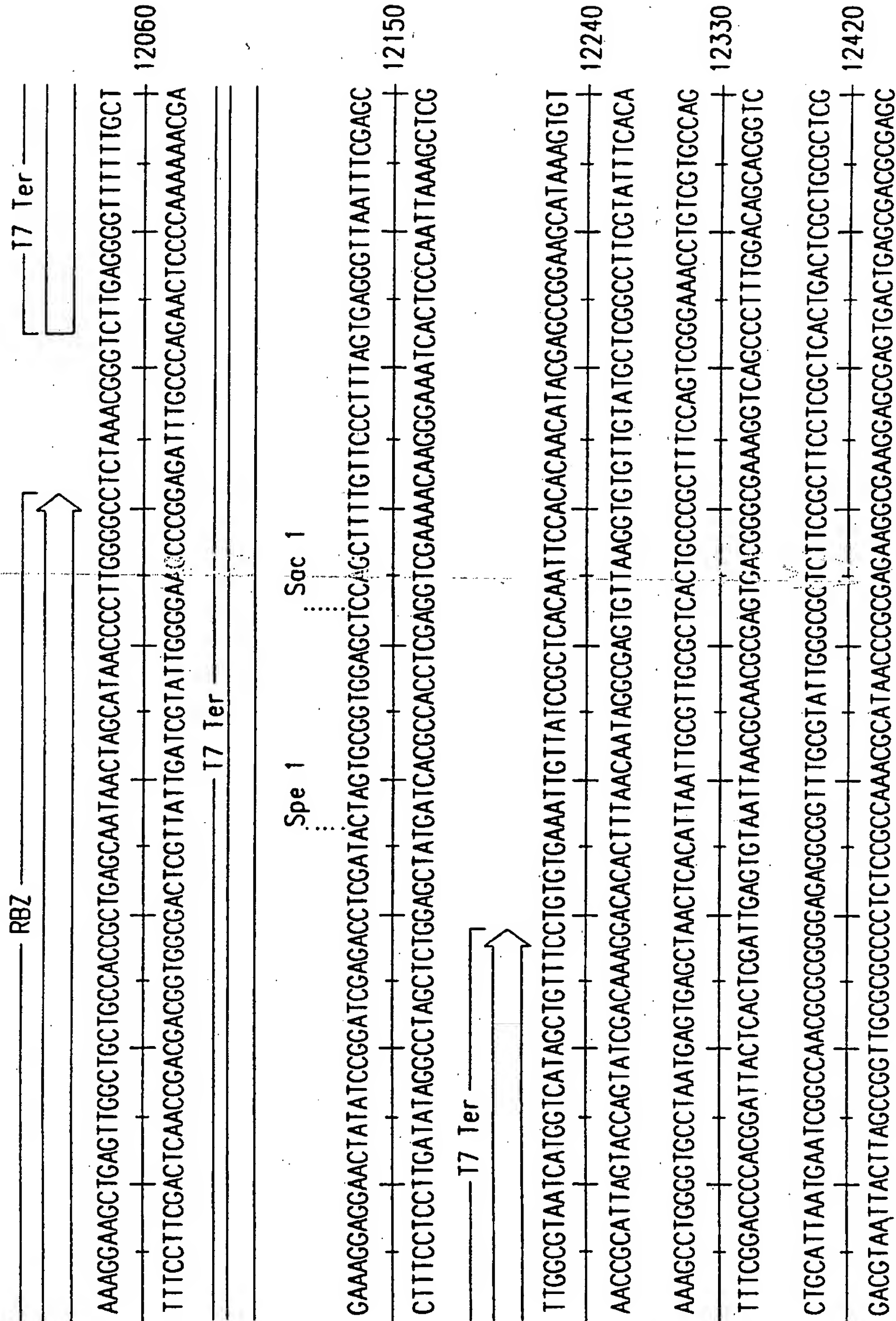


FIG. 1L1

39/50

GTCGTCGGCTCGCGGAGCGGTATCAGCTCAGTCAAGCGGTAAACGGTTATCCACAGAAATCAGGGGATAACGCAGGAAGAACATG 12510
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TGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAGGCCCGGTTCCTGGCGTTTTCATAGGCTCCGCCCCCTGACGAGCATCAC 12600
ACTCGTTTCCGGTCGTTTCCGGTCCTTGGCATTTTCCGGCGCAACGACCGCAAAAGGTAICCGAGCGCGGGGACTGCTCGTAGTG
AAAAATCGACCGTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACAGGCGTTTCCCCCTGGAAAGCTCCCTCGTCCGCTCT 12690
TTTTTAGCTGGAGTTCAGTCTCCACCGCTTTCGGCTGTCCTGATATTCTATGCTCCGCAAGGGGACCTTCGAGGGAGCACGGGAGA
CCTGTTCGGACCCCTGCGGCTTACCGGATACCTGTCCGCTTTCCTCCCTTCGGGAAACCGTGGGCTTCATAGCTACGCTGTTAGGTAT 12780
GGACAAGGCTGGGACGGCGAAATGGCTATGGACAGCGCGGAAGAGGGAAGCCCTTCGACCGCGAAAGAGTATCGAGTGGGACATCCATA
CTCAGTTCGGTGTAGGTGGTTCGCTCCAAGCTGGGCTGTGTGCAGCAACCCCGCTTCAGCCCGACCGCTCGGCTTAICCGGTAACTAT 12870
GAGTCAAGCCACATCCAGCAAGCGAGGTTCGACCCGACACACGTGCTTGGGGGCAAGTCCGGCTGGCGACCGCGGAATAGGCCATTGATA
CGTCTGAGTCCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACACCTGGTAACAGGATTAGCAGAGCGAGGTATGAGGCGGT 12960
GCAGAACTCAGGTTCGGCCATTCTGTCTGAATAGCGGTGACCGTGGTGGTACCATTGTCTTAATCGTCTCGCTCCATACATCCGCCA

FIG. 1M1

SUBSTITUTE SHEET (RULE 26)

40/50

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CGATGCTCAAGAAGTTCACCAACCGGATGATGCCGATGTAATCTCCCTGATTAACCATAGACGGAGACGACTTCGGTCAATGGAAG
13050

GGAAAAGAGTGGTAGCTCTTGATCCGGCAAAACACCGCTGGTAGCGGTGTTTTTTTGGTTTGGCAAGCAGCAGATTACGCCGCAGA
CCTTTTTCTCAACCATCGAGAACIAGGCCGTTTGTTGGTGGGACCATGCCCAACCAAAAACAAACGTTTCGTCTTAATGCGCGTCT
13140

AAAAAGGATCTCAAGAAGATCCCTTTGAATCTTTCTACGGGCTCGACCGCTCAGTGGAAACGAAACATCACGTTAAGGATTTTGGTTCATG
TTTTTTCCTAGAGTCTCTTAGGAAACTAGAAAAGATGCCCCAGACTCGGAGTCACCTTGCCTTTTGAGTGGCAATTCCTTAAACCAGTAC
13230

AGATTATCAAAAAGGATCTTCACCTAGATCCCTTTTAAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCT
TCTAATAGTTTTTCCTAGAAGTGGATCTAGGAAAAATTAAATTTTACTTCAAAATTTAGTTAGATTTCATATATATACATTTGAACCAGA
13320

GACAGTTACCAAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGCTATTTTCGTTTCATCCCATAGTTGCCCTGACATCCCGCTCGTGTAG
CTGTCAAATGGTTACGAAATTAGTCATCCGTGGATAGAGTCGCTAGACAGATAAAGCAAGTAGGTATCAACCGACTGAGGGCGCAGCACATC
13410

ATAACTACGATACGGAGGGCTTACCATCTGGCCCCAGTCTGCAATGATACCGGAGACCCACGCTACCGGCTCCAGATTTATCAGCA
TATIGATGCTATGCCCTCCCGAATGGTAGACCGGGTACCGACGTTACTATGCCCTCTCGGAGTGGCCGAGGCTCTAAATAGTCTGT
13500

ATAAACCAGCCAGCCGAAGGGCCGAGCGCAGAGTGGTCTTCCGAACCTTTATCCGCCCTCCATCCAGTCTAATTAATGTCGCCGGGAAGCT
TATTTGGTGGTCCGCCCTCCCGGCTCCCGGCTCCCGGCTCCCGGAGGCTGAAATAGCGGAGGCTAGGTCAGATAATTAAACAACCGCCCTTCGA
13590

FIG. 1N1

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AGAGTAAGTAGTTCGCCAGTTAATAGTTTGGCAACGTTGTIGCCATTGCTACAGGCA TCGTGGTGCACGCTCGTCGTTGGTATGGCT 13680
TCICATTCAACGCGGTCAATTATCAAAACGCGTTGCAACAACGTTACCGTAGCACACAGTCCGAGCAGCAAAACCATACCGA
TCATTCAGCTCCGTTCCCAACGAICAAGCGGAGTTACATGATCCCCCATGTGTGCAAAAAGCGTTAGCTCCTTCGGTCCCTCCGATC 13770
AGTAAGTCGAGGCCAAGGTTGCTAGTTCCGCTCAATGCTAGGCGGTACAACATGTTTTTCGCCCAATCGAGGAAGCCAGGAGGCTAG
GTTCAGAGTAAGTTCGCCCGCAGTGTATCAGCTCATGGTTATGCCAGCACGTATAATTCTCTTACTGTCTATGCCATCCGTAAGATGC 13860
CAACAGCTTTCATTCACCGCGGTACAAATAGTGAGTACCAATACCGTCGTGACLTATTAAAGAGAAAGACAGTACCGTAGGCATTCTACG
TTTTCTGTGACTGGTGGTACTCAACCAAGTCATTCIGAGAAATAGTGATCGCGGACCGAGTTCCTCTTCCCCGGCGTCAATACGGGAT 13950
AAAAGACACAGCACATCAGTGGTTCAGTAAGACTCTTATCACAATACCGCGCTGGCTCAACGAGAACGGGCCCGCAGTTATGCCCTA
AATACCGCGCCACATAGCAGAACTTTAAAAGTCTCATCATTCGAAACGTTCTTCGGGGCGAAACCTCAAGGATCTTACCGCTGTTC 14040
TTATGGCGCGGTGTAICGCTTGAATTTTCACGAGTAGTAACCTTTTGAAGAAGCCCGCTTTTGAGAGTTCCTAGAAATGCCGACAAC
AGATCCAGTTCGATGTAAACCACATCGTCCACCCCACTGATCTTCAGCACTTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAACAGGA 14130
TCTAGGTCAAGCTACATTTGGGTGAGCAGGTGGTTGACTAGAAAGTGAAGTGGTCCGAAAGACCCACATCGTTTTTGTCTCT

FIG. 101

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AGGCAAAATCCCGCAAAAAGGGAATAAGGCGCACACGGAATGTTGAATACTCATACICTTCCTTTTCAATATTATGAAGCATTIAT
+ 14220
TCCGTTTTACGGCGTTTTTCCCTTATTCGCCGTGTCCTTTACAACCTAAGAGTATGAGAAGGAAAAAGTTATAATAACTTCGTAAATA
CAGGGTTATTGTCCTCATGAGCGGATACATATTGAATGTTTAGAAAAATAACAAATAGGGTTCGCGCCACATTTCCCGGAAAAGTG
+ 14310
GTCCCAATAACAGAGTACTCGCCCTAGTATAAAGTTACATAAATCTTTTATTGTTTATCCCCAAGCGCGGTAAAGGGCCTTTTCAC
C + 14311
G

FIG. 1P1

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GAGTGGTATCCATCTTTCATTAAATTAAAGCACACCAAGAAAGACAGATTTATACAGACATAGAGATGAACCGACTTGGAAAGTAAC
CTCAACCATAGCTAGAAACGTAATTAAATTTCGGTGGTCTCTTTTCGTCGTAATATGTCGTCTACTTGGCTGAACCTTTCATTG

ArgValGlyIleHisLeuCysIleLysLeuLysHisThrLysLysArgGlnIleGlyrThrAspIleGluMetAsnArgLeuGlyLys *

[illegible]

SYNTHETIC DNA INSERT

G3' NON-CODING

POLYLINKER

ATCAACTTCGATACCAATGCTCAACAGCGCCCAATTATAATTGAGTTTTAA TTTTATGAAAAAACTAACAGCAATCAATGGAAGTCC
TAGTTGAACACTATGGTACGAGTTTCTCCGGAGTTAAATATAAAGTCAAAAAATTAATACTTTTTTIGATTGCTTAGTACCTTCAGG 5490

FIG. 2A

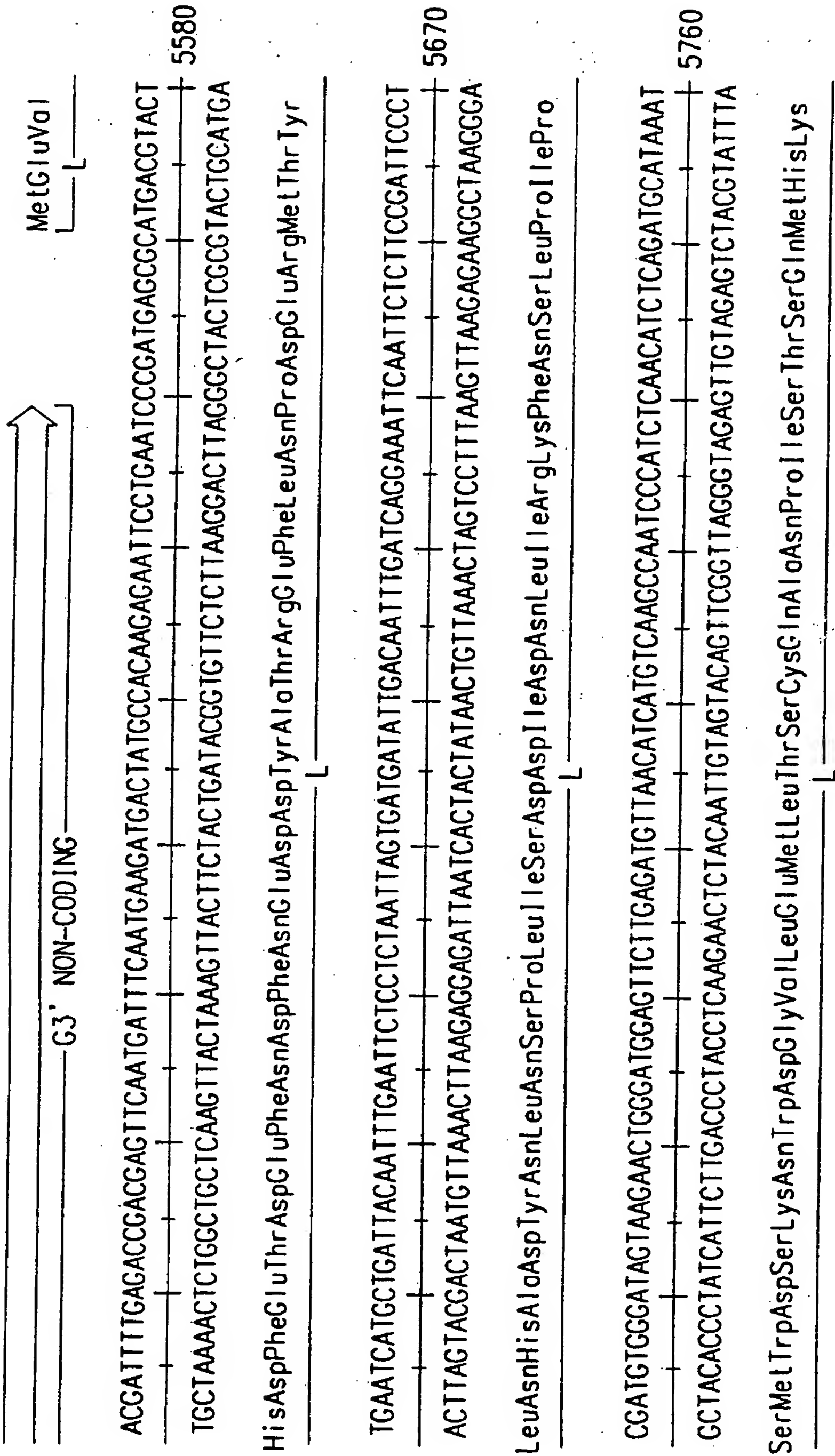


FIG. 2B

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		SEQUENCE IS NO:
LEADER RNA	5' ^I UCAGGAGAAAC ^{G_{PPP}} ^N AAACAGUAAUC 3'	15, 16
vRNA	3' AGUCCUCUUUGAAAUUGUCAUUAG 5'	17
mRNAs	5' ^N GCUACAU AUG-poly(A) ^{G_{PPP}} ^{NS} AAACAGUAAUC 3'	18, 19
vRNA	3' CGAUGUAUACUUUUUUUGAUUGUCUAUAG 5'	20
mRNAs	5' ^{NS} GUAGACUAUG-poly(A) ^{G_{PPP}} ^M AAACAGUAAUC 3'	21, 22
vRNA	3' CAUCUGAUACUUUUUUUCAUUGUCUAUAG 5'	23
mRNAs	5' ^M UAUCCCUAUG-poly(A) ^{G_{PPP}} ^G AAACAGAGAUC 3'	24, 25
vRNA	3' AUAGGGAUACUUUUUUUGAUUGUCUCUAG 5'	26
mRNAs	5' ^G AAUUUUUAUG-poly(A) ^{G_{PPP}} ^L AAACAGCAAUC 3'	27, 28
vRNA	3' UUA AAAAUACUUUUUUUGAUUGUCGUUAG 5'	29
mRNAs	5' ^L UUUAAGUAUG-poly(A)	30
vRNA	3' AA AUUCAUACUUUUUUUGAAACUAGGA 5'	31

FIG.3

SUBSTITUTE SHEET (RULE 26)

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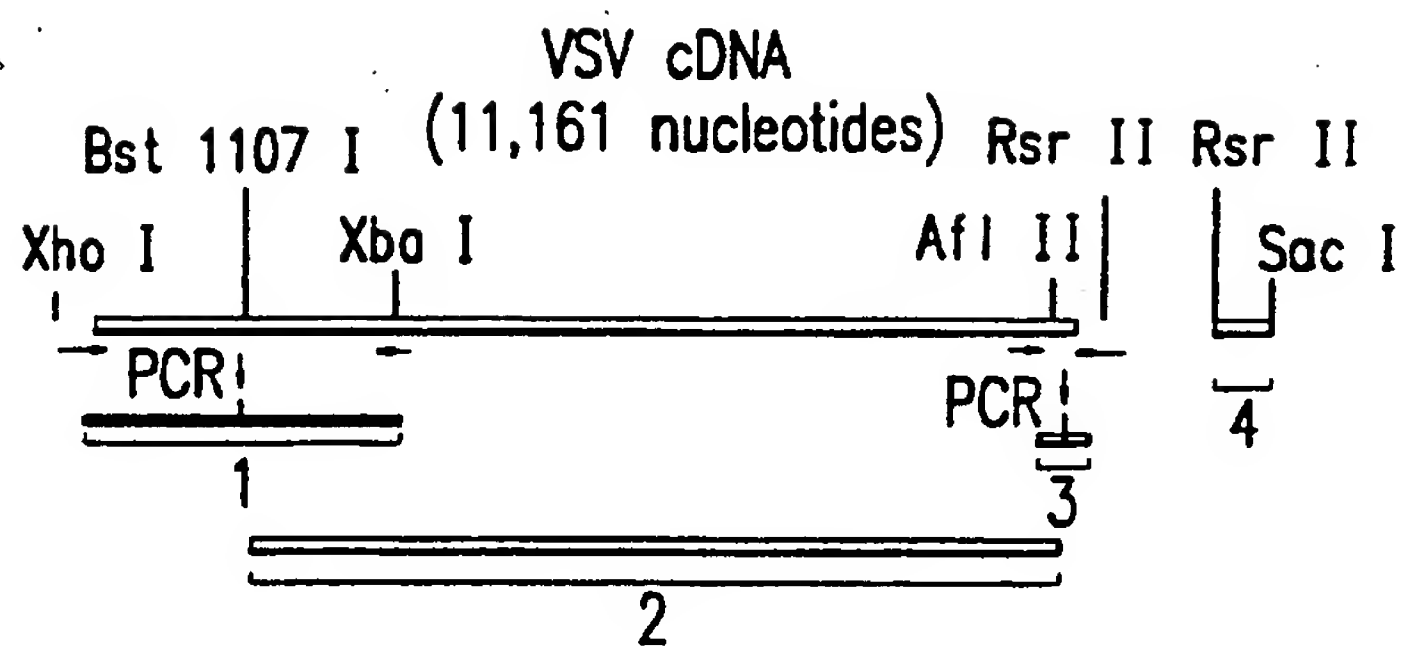


FIG.4A

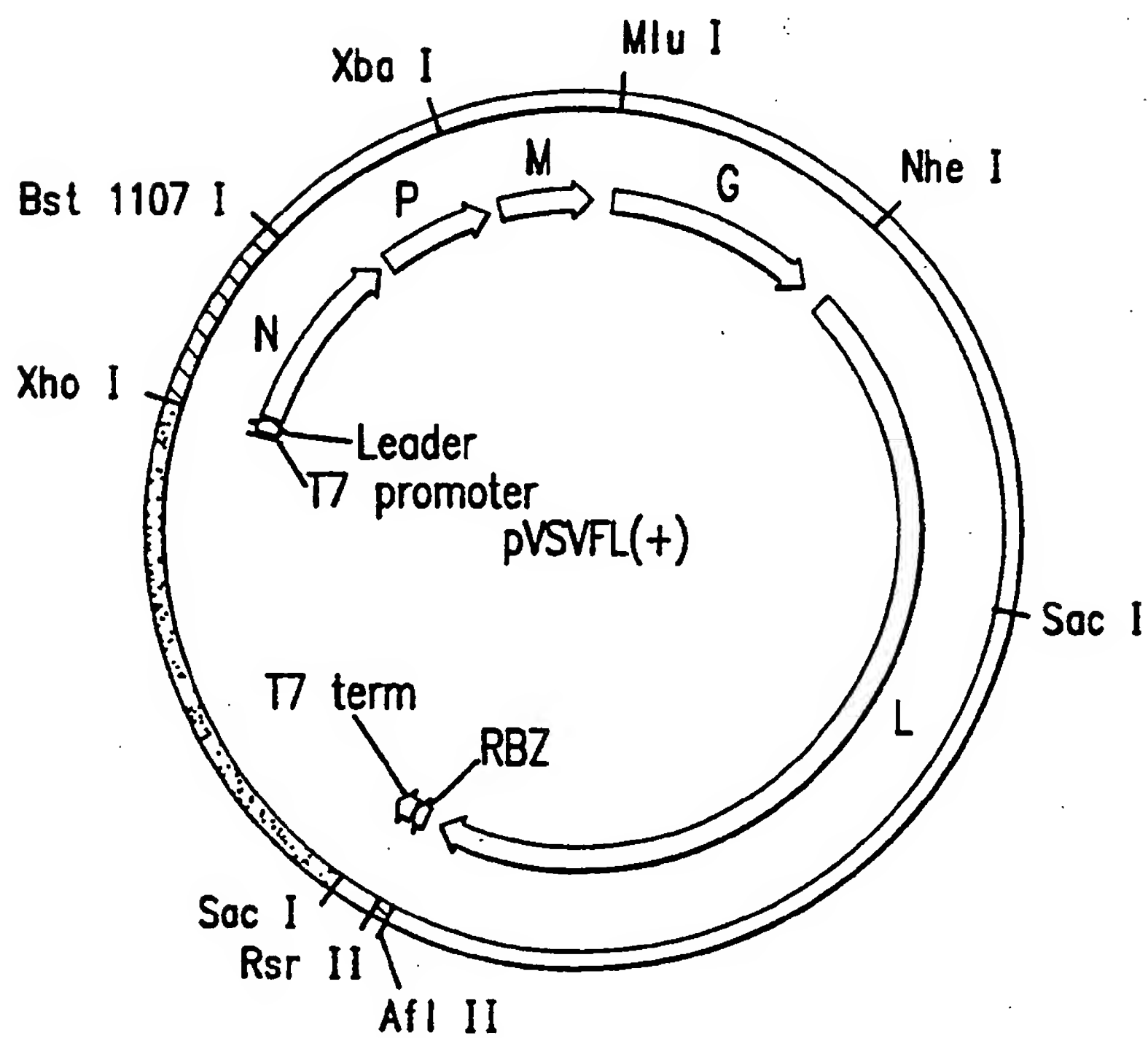


FIG.4B

SUBSTITUTE SHEET (RULE 26)

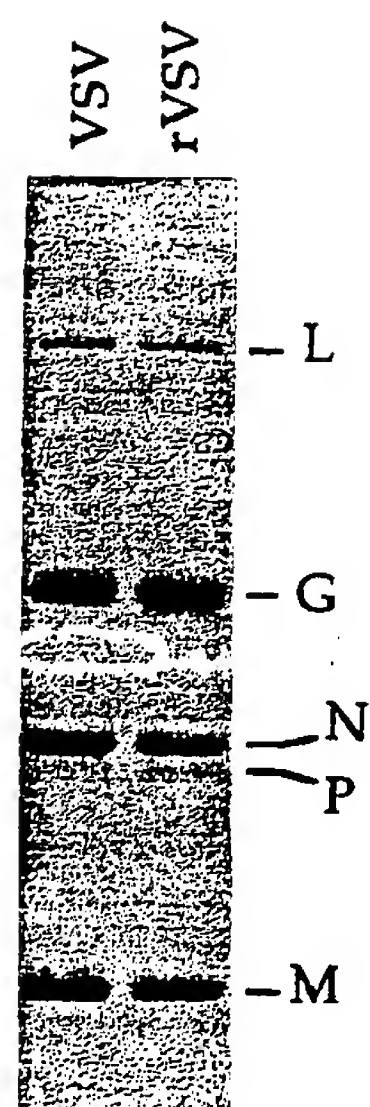


FIG. 5

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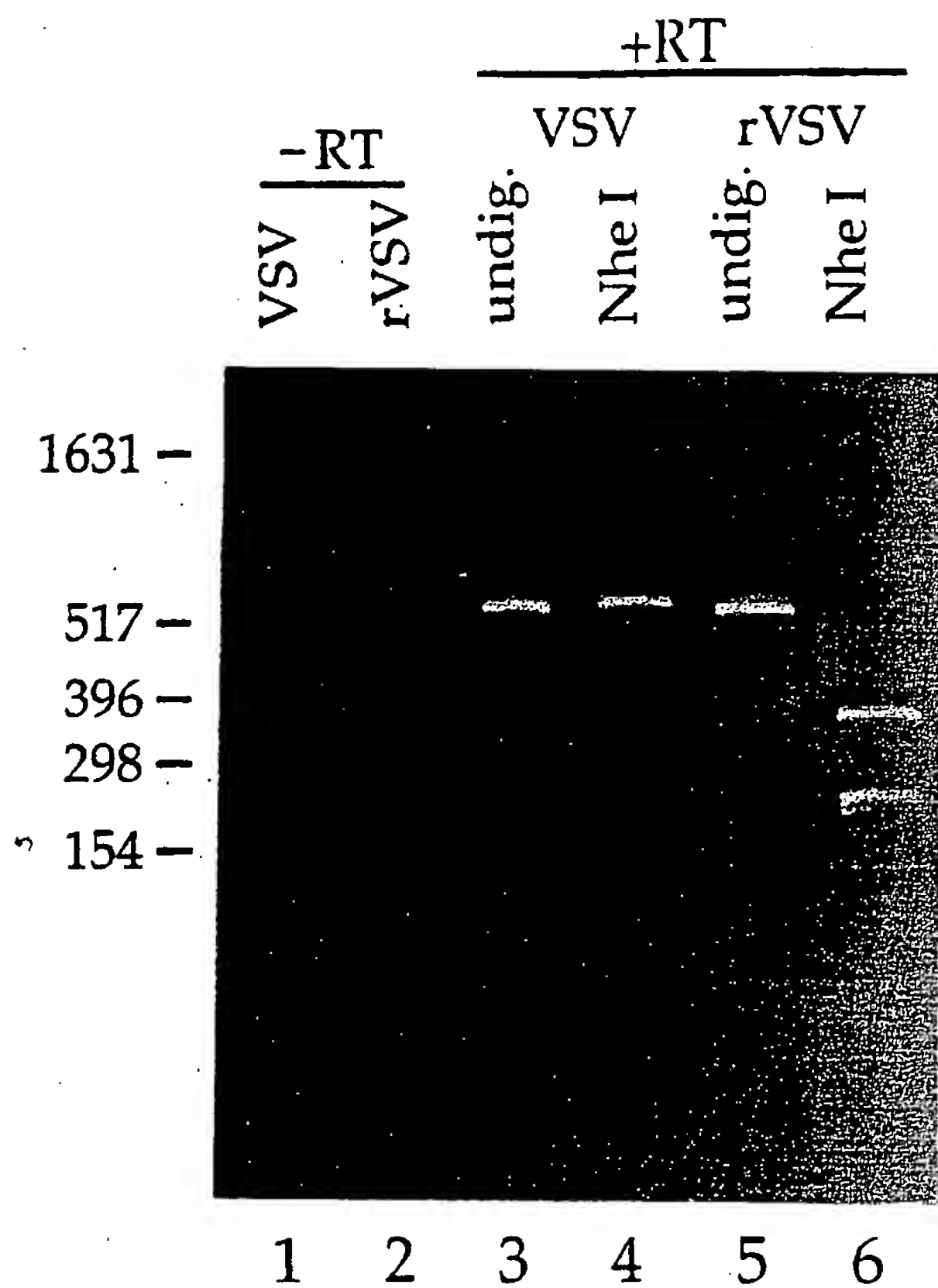


FIG.6

SUBSTITUTE SHEET (RULE 26)

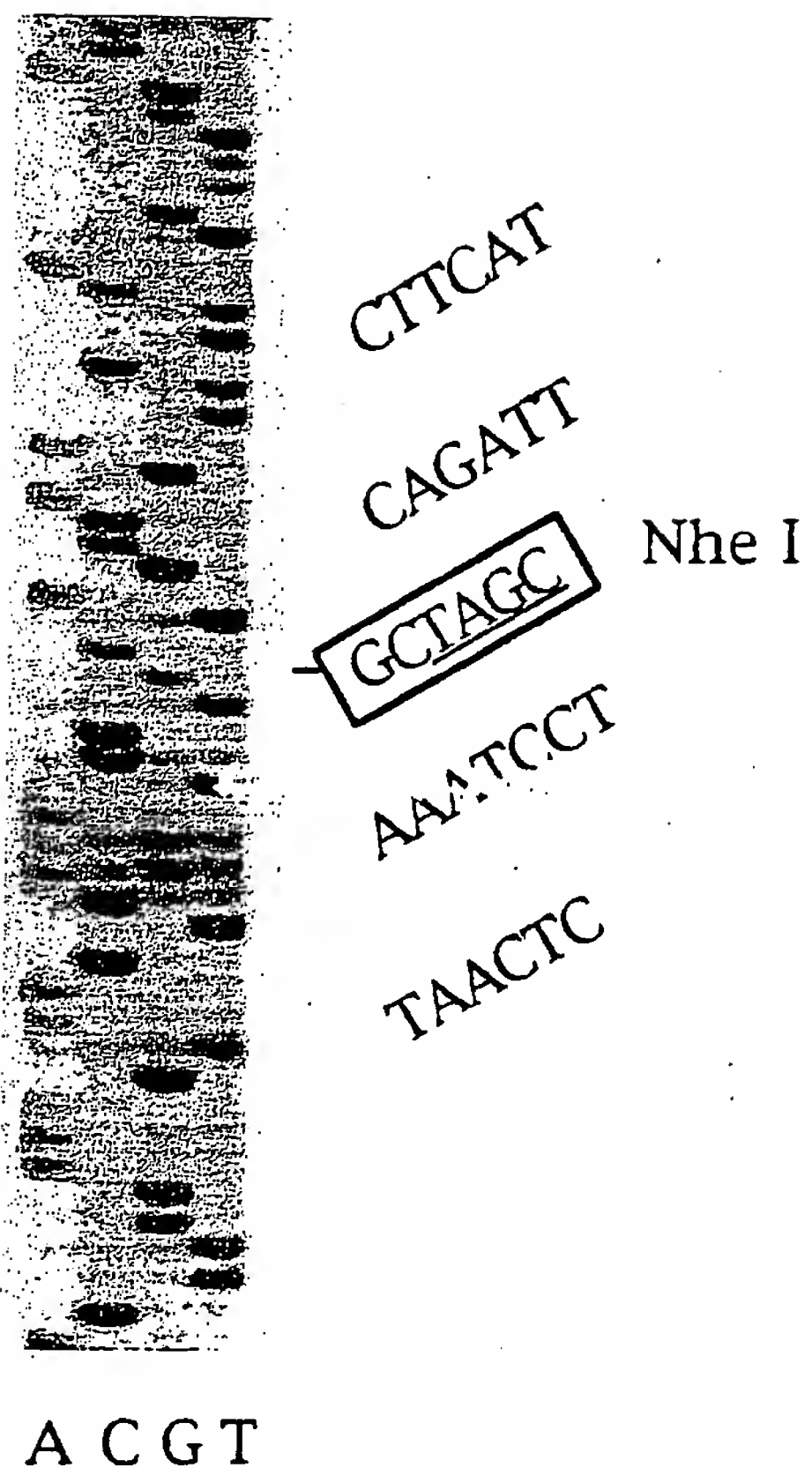


FIG.7

SUBSTITUTE SHEET (RULE 26)

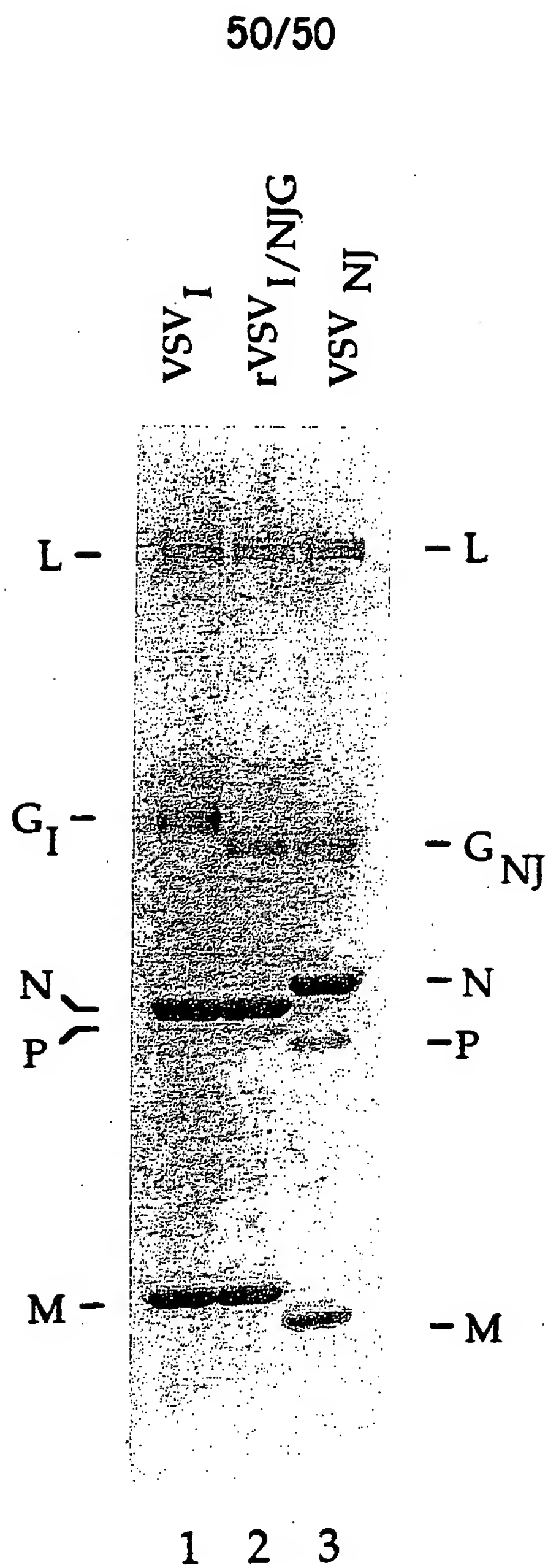
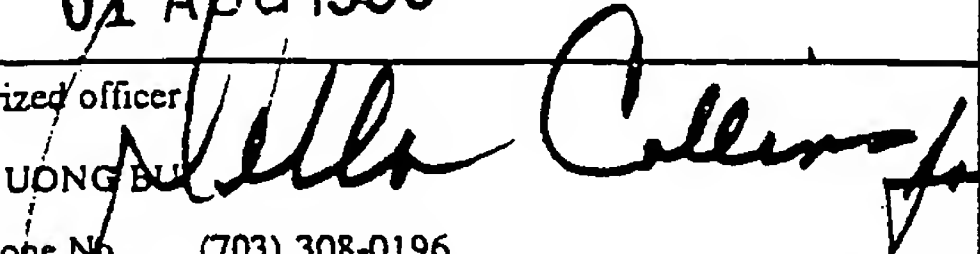


FIG.8

SUBSTITUTE SHEET (RULE 26)

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US96/06053

A. CLASSIFICATION OF SUBJECT MATTER IPC(6) : Please See Extra Sheet. US CL : Please See Extra Sheet. According to International Patent Classification (IPC) or to both national classification and IPC																				
B. FIELDS SEARCHED Minimum documentation searched (classification system followed by classification symbols) U.S. : Please See Extra Sheet. Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) APS, DIALOG (BIOSIS, DISSABS, EMBASE, MEDLINE, WPIDS)																				
C. DOCUMENTS CONSIDERED TO BE RELEVANT																				
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.																		
Y	US 5,166,057 A (PALESE et al.) 24 November 1992 (24/11/92), see entire document.	1-74																		
Y	SCHNELL et al. Infectious rabies viruses from cloned cDNA. The EMBO Journal. 1994, Vol. 13, No. 18, pages 4195-4203, see entire article.	1-74																		
Y	OWENS et al. Cytoplasmic domain requirement for incorporation of a foreign envelope protein into Vesicular Stomatitis Virus. Journal of Virology. January 1993, Vol. 67, No. 1, pages 360-365, especially abstract and discussion.	1-74																		
<input checked="" type="checkbox"/> Further documents are listed in the continuation of Box C. <input type="checkbox"/> See patent family annex.																				
<table border="0"> <tr> <td>* Special categories of cited documents:</td> <td>*T</td> <td>later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention</td> </tr> <tr> <td>*A* document defining the general state of the art which is not considered to be of particular relevance</td> <td>*X*</td> <td>document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone</td> </tr> <tr> <td>*E* earlier document published on or after the international filing date</td> <td>*Y*</td> <td>document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art</td> </tr> <tr> <td>*L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)</td> <td>*Z*</td> <td>document member of the same patent family</td> </tr> <tr> <td>*O* document referring to an oral disclosure, use, exhibition or other means</td> <td></td> <td></td> </tr> <tr> <td>*P* document published prior to the international filing date but later than the priority date claimed</td> <td></td> <td></td> </tr> </table>			* Special categories of cited documents:	*T	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention	*A* document defining the general state of the art which is not considered to be of particular relevance	*X*	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone	*E* earlier document published on or after the international filing date	*Y*	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art	*L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	*Z*	document member of the same patent family	*O* document referring to an oral disclosure, use, exhibition or other means			*P* document published prior to the international filing date but later than the priority date claimed		
* Special categories of cited documents:	*T	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention																		
A document defining the general state of the art which is not considered to be of particular relevance	*X*	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone																		
E earlier document published on or after the international filing date	*Y*	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art																		
L document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	*Z*	document member of the same patent family																		
O document referring to an oral disclosure, use, exhibition or other means																				
P document published prior to the international filing date but later than the priority date claimed																				
Date of the actual completion of the international search		Date of mailing of the international search report																		
27 JUNE 1996		01 AUG 1996																		
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231		Authorized officer																		
Facsimile No. (703) 305-3230		PHUONG BUI 																		
		Telephone No. (703) 308-0196																		

Form PCT/ISA/210 (second sheet)(July 1992)*

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US96/06053

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	SEONG, B.L. Influencing the Influenza Virus: Genetic Analysis and Engineering of the Negative-Sense RNA genome. Infectious Agents and Disease. 1993, Vol. 2, No. 1, pages 17-24, see entire article, especially conclusions, first paragraph, last sentence.	1-74
A	WHELAN et al. Efficient recovery of infectious vesicular stomatitis virus entirely from cDNA clones. Proc. Natl. Acad. Sci. USA. August 1995, Vol. 92, pages 8388-8392, see entire article.	1-74
A	COLLINS et al. Production of infectious human respiratory syncytial virus from cloned cDNA confirms an essential role for the transcription elongation factor from the 5' proximal open reading frame of the M2 mRNA in gene expression and provides a capability for vaccine development. Proc. Natl. Acad. Sci. USA. December 1995, Vol. 92, pages 11563-11567, see entire article.	1-74

Form PCT/ISA/210 (continuation of second sheet)(July 1992)*

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US96/06053

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

Please See Extra Sheet.

1. ☒ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

☐
☐

- The additional search fees were accompanied by the applicant's protest.
No protest accompanied the payment of additional search fees.

Form PCT/ISA/210 (continuation of first sheet(1))(July 1992)*

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US96/06053

A. CLASSIFICATION OF SUBJECT MATTER: IPC (6):

A61K 39/205
C07H 21/02, 21/04
C12N 5/10, 5/47, 7/01, 7/04, 15/01, 15/47, 15/63, 15/86
C12P 21/00

A. CLASSIFICATION OF SUBJECT MATTER: US CL :

424/199.1, 224.1,
435/69.3, 172.3, 235.1, 236, 239, 240.2, 320.1, 810
536/23.72

B. FIELDS SEARCHED Minimum documentation searched Classification System: U.S.

424/199.1, 224.1,
435/69.3, 172.3, 235.1, 236, 239, 240.2, 320.1
536/23.72

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING

This ISA found multiple inventions as follows:

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees must be paid.

I. Claims 1-10, 13-36, 39-43 and 51-59, drawn to recombinant vesiculoviruses, host cells, a first method of making recombinant vesiculoviruses, and a first method of using recombinant vesiculoviruses.

II. Claims 11-12, drawn to a second product, directed to a plasmid and a nucleic acid sequence.

III. Claims 37-38, drawn to a third product, directed to combination vaccines.

IV. Claims 44-50, drawn to a fourth product, directed to kits containing nucleic acids.

V. Claims 60-72, drawn to a fifth product, directed to inactivated vesiculoviruses, vaccines, kit and method of use.

VI. Claim 73, drawn to a second method, directed to a method of making viral proteins.

VII. Claim 74, drawn to a third method, directed to a method of making an inactivated vaccine.

The inventions listed as Groups I-VII do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons:

Inventions VII and V are related as process of making and product made. The inactivated vesiculoviruses of the claimed invention can be produced by using a variety of inactivating agents such as radiation, mutagenizing chemicals, or site-directed mutagenesis and are not so linked by special technical feature within the meaning of PCT Rule 13.2 so as to form a single general inventive concept.

Further, the products of Groups I, II, III, IV, and V differ one from another in their physical, chemical, and immunological properties such as chemical structure and composition, primary amino acid or nucleotide sequence, and antigenicity and immunogenicity and are not so linked by special technical feature within the meaning of PCT Rule 13.2 so as to form a single general inventive concept.

Further, the methods of Groups I, V, VI, and VII each differ one from another in method steps, reagents, and utility and are not so linked by special technical feature within the meaning of PCT Rule 13.2 so as to form a single general inventive concept.

Further, the products of groups I through IV and the methods of groups VI and VII are directed to independent inventions not so linked by special technical feature within the meaning of PCT Rule 13.2 so as to form a single general inventive concept.

